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Minimum DB
Maximum DB
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Perfect score:
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A_Geneseq_21:*
1: geneseqp1980s:*
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3: geneseqp2000s:*
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6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2005s:*
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length: 2000000000
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2670
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | ٠ د د | 222 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | a | ₅ | 4 | ൧ | þ | _ | Result No. |
|-----------|------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|--------------|----------|----------|----------|----------|---------------|
| 1010 | 1346 | 1360.5 | 1360.5 | 1444 | 1508.5 | 1529.5 | 1529.5 | 1534.5 | 1534.5 | 1534.5 | 1534.5 | 1534.5 | 1534.5 | 1534.5 | 1534.5 | 1534.5 | 1534.5 | 1580 | 1858 | 2409 | 2409 | 2499 | 2670 | Score |
| | 40.4 | • | • | 54.1 | 56.5 | 57.3 | 57.3 | 57.5 | 57.5 | 57.5 | • | • | • | | 57.5 | 57.5 | • | 59.2 | 69.6 | 90.2 | 90.2 | 93.6 | 100.0 | Query |
| j | 200 | 281 | 281 | 501 | 535 | 535 | 535 | 185 | 581 | 535 | 535 | 535 | 535 | 535 | 535 | 535 | 535 | 326 | 357 | 462 | 462 | 499 | 507 | Length |
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| TEOOTO | AEA61759 | ADI29262 | AAB65655 | AAB54157 | AAW77299 | AAG67420 | AAB92901 | ADI54546 | AAU87231 | AEA61758 | AD058699 | ADI29264 | ADG10732 | ADD47447 | ABB05696 | AAB93483 | AAB65657 | AAB66605 | AAM78691 | ADI29261 | AAB65654 | ADV97865 | ADJ96642 | ID |
| r.coarbou | Aea61759 | Ad129262 | Aab65655 | Aab54157 | Aaw77299 | Aag67420 | Aab92901 | Adi54546 | Aau87231 | Aea61758 | Ado58699 | Adi29264 | Adg10732 | Add47447 | Abb05696 | Aab93483 | Aab65657 | Aab66605 | Aam78691 | Adi29261 | Aab65654 | Adv97865 | Adj96642 | Description |
| Human | | Mouse | | Human | Amino | Amino | Human | Nove1 | • | Human | Human | Human | - | Human | Human | Human | | Human | Human | Human | Novel | Murine | Ħ | O B |
| 2 | anc anc | MAR | pro | pan | aci | aci | pro | hum | cen | nuc | reg | MAR | STA | Pro | bra | pro | pro | h15 | pro | MAR | pro | ם אם | Nim | |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ω | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 |
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| 395 | 395 | 395 | 395 | 395 | 395 | 396 | 756 | 756 | 756 | 756 | 882.5 | 946 | 946 | 946 | 946 | 951.5 | 1106.5 | 1106.5 | 1170 | 1174.5 |
| 14.8 | 14.8 | 14.8 | 14.8 | 14.8 | 14.8 | 14.8 | 28.3 | 28.3 | 28.3 | 28.3 | 33.1 | 35.4 | 35.4 | 35.4 | 35.4 | 35.6 | 41.4 | 41.4 | 43.8 | 44.0 |
| 2245 | 2219 | 2217 | 2193 | 1345 | 779 | 2091 | 302 | 302 | 302 | 302 | 752 | 340 | 340 | 340 | 340 | 308 | 378 | 378 | 293 | 637 |
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| ADJ96651 | ADN00364 | ADX98203 | ABR42219 | AAE25097 | ABB97147 | ADN61449 | ADI54547 | ADB93965 | AAU87232 | AAU17257 | ADC87261 | ADI54850 | ADB93941 | AAU87535 | AAU17233 | AAB36408 | ADI29265 | AAB65658 | ABP96552 | ABB57826 |
| Adj 96651 | Adn00364 | Adx98203 | Abr42219 | Aae25097 | Abb97147 | Adn61449 | - | - | | Aau17257 | | Adi54850 | Adb93941 | Aau87535 | Aau17233 | Aab36408 | Adi29265 | Aab65658 | Abp96552 | Abb57826 |
| Human Nim | Novel hum | Lysine de | Human pro | Human kin | Human tum | Human KPP | Novel hum | | | Novel sig | | Novel hum | Human nov | Novel cen | Novel sig | Secreted | Mouse | Novel | | Drosophil |

ALIGNMENTS

RESULT 1 ADJ96642 ID ADJ9 kinase; human; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; antiinflammatory; enzyme; Nim-A related protein kinase; NRBP2. Human Nim-A related protein kinase NRBP2 protein SeqID 06-MAY-2004 ADJ96642 standard; protein; 507 AA. 22-JAN-2004. WO2004006838-A2 Homo sapiens. ADJ96642; (first entry) 99

15-JUL-2003; 2003WO-US021730. L5-JUL-2002; 2002US-0395632P.

Whyte D, Manning G, Caenepeel S;

(SUGE-) SUGEN INC.

WPI; 2004-122753/12. N-PSDB; ADJ96576.

New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., coor neurological, immunological or inflammatory disorders. cancer,

Claim 1; SEQ ID NO 99; 366pp; English.

This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enraymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy

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RESULT 2
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Matches 507
                                  enzyme; protein kinase modulator; bioinformatics; diagnostic; cancer; central nervous system disease; psychotic disorder; neurological disorder; neurological disorder; neurological disorder; neurological disorder; cardiovascular disease; inflammatory disorder; gene therapy; cytostatic; antimigraine; analgesic; endocrine-gen; nootropic; tranquilizer; hypotensive; neuroprotective; antiparkinsonian; virucide; fungicide; antibacterial; antidiabetic; anorectic; antitarteriosclerotic; ophthalmological; antiinflammatory; antiarthritic; antirheumatic; antitatediabetic; antiasthmatic; osteopathic; antipsoriatic; immunosuppressive; cardiovascular-gen.; vasotropic; antiallergic; gastrointestinal-gen.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cycostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polypeptide sequence is a human kinase protein sequence of the invention.
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This invention relates to novel isolated, enriched or purified nucleic CC acid molecules that encode kinase polypeptides. Specifically, it refers CC to a biolinformatics strategy used to identify mammalian members of the CC protein and lipid kinase families. The present invention provides methods CC for identifying a substance that modulates the activity of a kinase cC polypeptide, as well as a method for the detection of a kinase nucleic acid in a sample as a diagnostic tool for a disease or disorder. CC Furthermore, it describes generation of a knock-out mouse whose genome is CC disrupted by recombination at a nucleic acid sequence such that it CC produces a phenotype, relative to the wild-type, that exhibits an absence CC of kinase activity. The nucleic acids and polypeptides given in the Specification are useful for the diagnosis and treatment of cancer, CC cardiovascular disease or inflammatory diseases, psychotic and neurological CC disorders, neuropeses and compositions exhibit cytostatic, CC antinigraine, analgesic, endocrine-Gen., nootropic, tranquilizer, CC inputensive, hypertensive, neuroprotective, antiparkinsonian, virucide, CC antiasthmatic, osteopathic, antidabetic, amorectic, antiarteriosclerotic, CC antiasthmatic, osteopathic, antipartiari, immunosuppressive, cardiant-CC gen, vasotropic, antiallergic and gastrointestinal-gen. This polypeptide is a murine protein kinase of the invention.
                Query Match
                                                     Sequence 499
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TAVDIFSFGMCALEMAVLEIQANGDTRVTEEAIARARHSLSDPNMREFILSCLARDPARR
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Pred. No. 5.5e-
11; Mismatches
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Local

Similarity

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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase cardiovaty include rheumatoid arthritis, atherosclerosis, autoimmune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, cardiomyopathies, strokes, renal failure, oxidative-integen also cardiomyopathies, strokes, renal failure, oxidative-integen related disorders, chronic inflammatory polvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                         neurodegenerative diseases and/or cancers
                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF44681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
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Best Local Similarity
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 ADI29261 standard;
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                                                                                 LTYDLLPTDSAQDLASELVHYGFLHEDDRMKLAAFLESTFLKYRGTQA
                                                                                                                                                                                             EKTKAMDLHAVLABLPRPRRPPLOWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGL
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protein;
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No. 2.
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RESULT 4
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Best Local Similarity
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                  Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification.
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                                                                    SEQ ID NO 1353.
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Pred. No. 2.9e-225;
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAW78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiseis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111 (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang
Ma Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                              Sequence 357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding in diagnosis and gene t
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Y, Zhao QA,
AJ, Yang Y,
                                                                                                                                                                                                                                 145
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                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYSEQ INC.
                                                                                                                                                              PPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNG
IYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSETRKVIQMQCNLERSEDKARW
                                                  CFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRPPLQWRYSEVSFMELDKFLEDVRNG
                                                                                                         DTRVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAH
                                                                                           DTRVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAH
                                                                                                                                                -ALPODURSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNG
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; 2000US-00598075.
; 2000US-00620325.
; 2000US-00634936.
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; 2000US-00693325.
; 2000US-00693325.
                                                                                                                                                                                                                                                        Conservative
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Wejhrman
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                                                                                                                                                                                                                                                                     69.6%;
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Pred. No. 9.4e-172;
1; Mismatches 1;
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g J, Zhang J,
Goodrich R;
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J, Ren F,
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Best Local
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                                                                                                                                                                                                                                    Sequence 326 AA;
                                                                                                                                                                                                                                                                    The present invention relates to human protein kinase. The proteins are from new human genes termed h12832, h14138, h14933, h15990, h15993, h16341 and h2252. The proteins may be used to identify modulators of their activity. The proteins may also be used to derive products for the treatment of cellular growth related disorders, malignancies, cancers, immune, inflammatory, respiratory, haematological and bone-related
                                                                                                                                                                                                                                                                                                                                                                                 New protein kinase polypeptides, nucleic acids and anti-kinase antibodies, useful for diagnosing and treating e.g. cancer, in immune, cardiovascular and bone disorders.
                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hodge MR,
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01-MAY-2000; 2000US-00562480
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respiratory; haematological; bone disorder.
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IFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPBYGEVADG
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                                                                                                                                    MAAPEPAPRRAREREREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMD
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                                                            FITEYVSSGSLKOFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDT 180
                                                                                     TEEGVEVVMNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVI
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Pred. No. 1e-144;
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                                          The present sequence is a novel protein kinase. The novel protein kinases CC and the nucleic acids that encode them may be used in the treatment and CC diagnosis of diseases associated with inappropriate kinase expression Such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and disorders, cardiovascular disease, CC neurodegenerative diseases and/or cancers. The nucleic acids and CC complementary sequences may also be used as DNA probes in diagnostic assays. The kinase expression and activity. Anti-kinase antibodies CC assays. The kinase expression and activity. Anti-kinase antibodies CC and kinase antagonists may also be used to down regulate kinase CC expression and activity. Diseases related to kinase expression and CC immune disorders, complications of organ transplantation, myocardial infarction, transplantation, myocardial infarction, correct constructs related disorders, cardiomyopathies, strokes, renal failure, oxidative-current construction, pervised disease, multiple sclerosis, autoimmune osteoarthritis, portlasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                                      Claim 10; Fig 1; 310pp;
                                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative diseases and/or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding kinase polypeptides, useful for diagnosing treating immune-related diseases and disorders, cardiovascular dis
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immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-032161/04.
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Query Match Best Local Similarity

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09-JUN-2000;
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11-JAN-2000;
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Sugiyama T, Wakamats
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99JP-00300253.
2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
for synthesizing polynucleotides, particularly the 5602 full-
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                                                                                                                                                                                       detection; diagnosis; antisense therapy; gene therapy
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                                  Wakamatsu
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                                Saito K,
C, Otsuki
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length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs.
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aim 8; SEQ ID NO 12777; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full-CC length cDNAs defined in the specification. Where a primer set comprises:

((a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide comprises a 3'-end sequence complementary to a coligonucleotide which comprises a 3'-end sequence complementary to a coligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, and coligonucleotides, and coligonucleotides, and coligonucleotides, and coligonucleotides, and coligonucleotides, all of which are used in antisense therapy and in coligonucleotides, and coligonucleotides, all of which are used methods. AAH33623 to AAH3628 and coligonucleotides, all of which are used in the exemplification of the cDNAs. The primers are also was a special sed methods. AAH33629 to AAH3628 and coligonucleotides, all of which are used in the exemplification of the cDNAs.

Sequence 535 AA;

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Query Match
Best Local Similarity
Matches 305; Conser
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QSRLTSLLEETLNKF
                                                                                                                                                                                  LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEV-----QKAKTPTPEPFDSETRK
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                                                                                                                                                                                                                                                                                                                                       AVLEIQINGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE 314
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                                    RMKLAAFLESTFLKY 502
                                                                                                  VIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHEDD
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                                                                           VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD
                                                                                                                                                         LDKFLEDVRNGIYPLTAF-----GLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRK
                                                                                                                                                                                                                                   VPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQTLYSQSPALE
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                                                                                                                                                                                                                                                                                                                                                                                              -----APDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.5%; Score 1534.5; DB 4; 61.6%; Pred. No. 5.6e-140; cive 59; Mismatches 102;
518
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                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                         The present invention describes assemblages and computer readable media comprising novel human cDNA sequences and clones derived from human foetal brain, foetal kidney, melanoma, testis and amygdala cDNA libraries. ABA93702 to ABA93766 represent human cDNA sequences from the present invention which encode the proteins given in ABB0562 to ABB05729. The human cDNA sequences and clones can be used in gene therapy. The clones may be used in a variety of applications, for example they may be used in profiling assays, for providing large arrays of human genetic material for implementing large-scale screening strategies and for treating diseases via gene therapy procedures
                                                                                                                                                                                                                                                                                                                                                    Sequence 535 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA sequences and kidney, melanoma, testis
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                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                    RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM 255
                                                                                                                                                                                                               RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 216-217; 611pp;
                          AVLETQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFE
                                                                                                                                   KTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV--
                                                                                                                                                                                      RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK
                                                  AVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLPHRVLFE
                                                                              -----APDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEM
                                                                                                                                                            KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196
                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clones derived from human fetal brain, and amygdala cDNA libraries, useful in
                                                                                                                                                                                                                                                                                               59;
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                                                                                                                                                                                                                                                                                                             Score 1534.5; DB 5; Pred. No. 5.6e-140;
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RESULT 10
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                  The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, comprisitive or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a compound that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound that regulates the activity of one or more of the contribution of an animal of one or more of the contribution in the contribution of activity in an animal of one or more of the contribution in the contribution of activity in an animal of one or more of the contribution in the contribution of the contribution of the contribution of the contribution in the contribution of the contribution of the contribution of the contribution of the contribution in the contribution of 
activity in an animal of one or more of the polypeptides given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-268312/26.
GENBANK; NP_037524.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Woolf C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEHO )
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segmental nerve injury; chronic cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nerve injury; SNI; Chung.
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BAYER AG.
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                                                                          Human; STAT6-activating protein; drug screening; activator; inhibitor; allergic disease; inflammation; autoimmune disease; diabetes; hyperlipidaemia; cancer; infection; HIV infection; hyperfunction; human immunodeficiency; cancer; Thi hyperfunction; antiallergic; antiinflammatory; antidiabetic; antilipaemic; antiinfective; anti-HIV;
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CC encoding them (ADG10411-ADG10894) and to sequences with 95% or more CC homology to the STAT6-activating proteins and their encoding nucleic CC acids. The invention also relates to recombinant vectors and host cells CC comprising a STAT6-activating protein-encoding nucleic acid; the CC recombinant production of a STAT6-activating protein; antisense oligonucleotides and cribozymes targeted to nucleic acids encoding a STAT6-activating protein; CC methods of screening for activators or inhibitors of STAT6-activating protein; cc methods of screening for activators or inhibitors of STAT6-activating protein activating compositions comprising a modulator of STAT6-activating protein activating or expression; and methods of treating patients by CC administration of the drug compositions. The STAT6-activating proteins, CC nucleic acids encoding them, and modulators of their activity or expression and methods of treatment of allergic conjugations. The strategic patients of the conjugation of the diagnosis and treatment of allergic conjugations. The strategic patients of concer, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, CC cancer, infections (e.g., HIV), cancer and disorders associated with Thi CCC hyperfunction. The present sequence is related to the invention.
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                                                                                                                                                                                                                                                                                                                                                           EBEEESEDESEILEESPCGRWQKRREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSE
                                                                                                                                                                                                                                                                                                                                                                                  EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD
                                                                                                        AVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE
VPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQTLYSQSPALE
                                                                                                                                                                                                                  KTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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2001JP-00260681.
2001JP-00313175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         relates to 242 human STAT6-activating proteins (ADG10411-ADG10894) and to sequences with 95%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 1534.5; DB 7; Pred. No. 5.6e-140; 59; Mismatches 102;
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RESULT 12
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Query Match
Best Local Similarity
Matches 305; Conserv
                                                                                                  The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinse 3), that specifically hybridises with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative diseases. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                       New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                             Sequence 535 AA;
                                                                                         specification.
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-052188/05.
N-PSDB; ADI29382.
                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 184; 233pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antisense gene therapy; MARK3; MAP/microtubule affinity-regulating kinase 3; cancer; Alzheimer's disease; neurodegenerative disorde;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI29264 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MARK3-associated protein
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   Conservative
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               57.5%; Score 1534.5; DB 8; 61.6%; Pred. No. 5.6e-140;
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   Mismatches
   102;
   Indels
                             Length
                              535;
   29;
 Gaps
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cancer and

immune disorders.

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RESULT 13
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                                      WPI; 2004-459763/43.
N-PSDB; ADO58748.
                                                                      Guegler
                                                                                 Lal P,
                                                                                                                                    23-SEP-1997;
20-JAN-1999;
                                                                                                                                                                    26-SEP-2001; 2001US-00840787
                                                                                                                                                                                                               US2002058264-A1
                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                      cytostatic; immunomodulator; agonist; antagonist; gene therapy; human regulatory molecule; HRM; disease development; cell proliferation; immune response; cancer.
                                                                                                                                                                                                                                                                                                   Human regulatory molecule HRM-20
                 New human regulatory molecules,
                                                                                                                                                                                           16-MAY-2002
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                                                                                                      INCYTE PHARM INC
                                                                      Hillman JL,
KJ, Corley
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                                                                     Corley
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                                                                                                                                    97US-00933750.
99US-00234613.
                                                                                                                                                                                                                                                                                                                                                                  protein;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes human regulatory molecules (HRM) (I) selected CC from a group comprising the fully defined amino acid sequences of SEQ ID CC NOs: 1-49. Also described are: an isolated polynucleotide (II) comprising CC a nucleic acid sequence encoding (I) or the complement of the polynucleotide (SEQ ID NOs:50-98); a composition comprising (II) and a creporter molecule; an expression vector containing (II); a host cell containing the vector; detecting (M1) expression of a nucleic acid in a cc sample; screening (M2) a plurality of molecules to identify a ligand; CC dagnosing (M3) a disease associated with gene expression in a sample containing nucleic acids; a composition comprising (I) and a plurality of molecules to identify a plurality of molecules to identify a ligand; proparation and purification of antibodies; an antibody which specifically binds to (I); and detecting protein expression in a sample. The new human regulatory protein compositions which are useful in the diagnosis and treatment of disease associated with cell proliferation, particularly immune cremitatory and cancers. This is the amino acid sequence of a human regulatory compositions which are useful in the diagnosis and treatment of disease associated with cell proliferation, particularly immune
 11-AUG-2005
                                       AEA61758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 535 AA;
                                                                            AEA61758 standard;
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                                                                                                                                                                                                         RMKLAAFLESTFLKY
                                                                                                                                                                                                                                                                                 VIQMOCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHEDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----APDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEM
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 (first entry)
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                                                                          protein; 535
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77 44 17

RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK

163

76

RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK 136 EEEEESEDESEILEESFCGRWQKKREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSE EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD

KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196

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The present sequence is the protein sequence of human nuclear receptor CC binding protein (NRBP), a ubiquitously expressed, multidomain adapter CC protein. The inventors have discovered genes that modify the RAC GTPase CC pathway in Caenorhabditis elegans and identified their human orthologs as CC NRBPs. The invention provides methods for using these RAC modifier genes CC and polypeptides to identify NRBP-modulating agents that are candidate CC therapeutic agents that can be used in the treatment of disorders CC associated with defective or impaired RAC function and/or NRBP function. Preferred NRBP-modulating agents are CC and restore RAC function. Other preferred NRBP-modulating agents are CC uncleic acid modulators such as antiense oligomers and RNAi that repress CC mucleic acid modulators such as antiense oligomers and RNAi that repress CC waluated by in vitro or in vivo assay for molecular interaction with an RRBP polypeptide or nucleic acid. Agents that produce a change in the CC activity of there assay system relative to controls are identified as CC candidate RAC modulating agents. The assay system may be cell-based or CC cll-free. NRBP modulating agents include NRBP-related proteins (e.g. CC cll-free. NRBP modulating agents include NRBP-related proteins (e.g. CC cll-free. NRBP modulating agents include NRBP-related proteins (e.g. CC compete with an NRBP binding partner. The assay system may be call-based or CC compete with an NRBP binding partner. The screening assay may be an CC compete with an NRBP binding partner. The screening assay may be an CC compete with an NRBP binding partner. The screening assay or a hypoxic induction assay. A method for diagnosing a disease, especially XX
    Matches
                        Best Local Similarity
                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a candidate RAC pathway modulating agent using a nuclear receptor binding protein (NRBP) polypeptide or nucleic acid, useful for diagnosing or treating cancer.
                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 3; 51pp; English.
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N-PSDB; AEA61756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear receptor binding protein; GTPase modulator; cancer; cytostatic; gene therapy; antibody therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-2003; 2003US-0524541P
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305;
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  Conservative
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                      57.5%;
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Pred. No. 5.6e-140;
  Mismatches
                                         DB 9;
Indels
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Gaps
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AU8723

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       31-JAN-2000

04-FEB-2000

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26-JUL-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therany
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7 2000US-0184664P.
7 2000US-0184654P.
7 2000US-0186350P.
7 2000US-0199076P.
7 2000US-0199076P.
7 2000US-0299133P.
7 2000US-0299467P.
7 2000US-0214886P.
7 2000US-0215135P.
7 2000US-021647P.
7 2000US-021647P.
7 2000US-021649P.
7 2000US-0217496P.
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22-AUG-2000
22-AUG-2000
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14-AUG-2000;
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2000US-0227009P.
2000US-0229343P.
2000US-0229343P.
2000US-0229343P.
2000US-0230433P.
2000US-0231244P.
2000US-0231413P.
2000US-0231413P.
2000US-0231413P.
2000US-0231413P.
2000US-0231413P.
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2000US-0232081P.
2000US-023239P.
2000US-023239P.
2000US-023239P.
2000US-0232401P.
2000US-0232401P.
2000US-0233409P.
2000US-0233409P.
2000US-02342498P.
2000US-0235836P.
2000US-0236369P.
2000US-024684P.
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2000US-0225270P.
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2000US-0225757P.
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2000US-0227182P
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The invention describes an isolated nucleic acid molecule (I) encoding a covel central nervous system protein. (I) and polypeptides (III) encoded (I) are used to treat a medical conditions and in diagnosis of a CC pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative (I) disorders e.g. neoplasms of the breast or liver, cardiovascular disorders (I) cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (I) angiogenesis, nervous system disorders e.g. Alzheimer's disease and (I) amylotrophic lateral sclerosis, infections caused by bacteria, viruses (I) amylotrophic lateral sclerosis, infections caused by bacterial viruses (I) c.g. corneal infection, gastrointestions and fungi, ocular disorders (I) c.g. corneal infection, gastrointestinal disorders e.g. dysphagia, (I) disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes (I) calcars (I) calcars (I) cancers and disorders at the cellular level e.g. cleukaemia, disorders involving neovascularisation e.g. malignancies,
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17-NOV-2000,
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06.DEC-2000;
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                                                                                                                                                                                                                                                                nucleic acid encoding a protein for diagnosing, ameliorating medical conditions and used as food
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QSRLTSLLEETLNKF
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ALIGNMENTS

| AR448352 | | | | | | | |
|------------------------|------------------------|---|--------------------------|-----|---------|------|-----------------|
| Locus | AR448352 | 4 | 4048 bp DNA | | linear | PAT | PAT 20-FEB-2004 |
| DEFINITION | Sequence 109 | Sequence 1053 from patent US 6673549 | US 6673549. | | | | |
| ACCESSION | AR448352 | • | | | | | |
| VERSION | AR448352.1 GI:42676676 | GI:42676676 | | | | | |
| KEYWORDS | • | | | | | | |
| SOURCE | Unknown. | | | | | | |
| ORGANISM | Unknown. | | | | | | |
| | Unclassified. | | | | | | |
| REFERENCE | 1 (bases 1 to 4048) | to 4048) | | | | | |
| AUTHORS | Furness, L.M. | Furness, L.M. and Buchbinder, J.L. | er,J.L. | | | | |
| TITLE | Genes expres | Genes expressed in C3A liver cell cultures treated with steroids | ver cell cultu | res | treated | with | steroids |
| JOURNAL | Patent: US 6 | Patent: US 6673549-A 1053 06-JAN-2004; Incyte Corporation: Palo Alto. CA | 06-JAN-2004; Alto. CA | | | | |
| FEATURES | Loc | Location/Qualifiers | ers | | | | |
| source | - | 4048 | | | | | |
| | to/ | /organism="unknown" | wn" | | | | |
| | /mc | /mol_type="genomic DNA" | ic DNA" | | | | |
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| Pred. No.: | | 1.16e-213 | Length: | | 4048 | | |
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                                                                                                                          SerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspProAlaArgArg
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                                                                              ProSerAlaHi8SerLeuLeuPheHi8ArgValLeuPheGluValHi8SerLeuLy8Leu
                                                                                                              AGTGACCCCAACATGCGGGAGTTCATCCTTTGCTGCCTGGCCCGGGACCCTGCCCGGC
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                       CTGGCAGCCCACTGCTTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAGGAG
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 Strausberg, R.
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RS Strausberg, L. Gollins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Booak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Boutfard, G.G., Blakesley, R. W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schmerch, A., Schein, J.E., Jones, S.J. and Mazra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Homo sapiens hypothetical protein LOC340371, mRNA (cDNA
IMAGE:4375917), partial cds.
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Mammalia; Eutheria;
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1 (bases 1 to 3892)
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| | US-10-618-941-99 (1-507) x BC071605 (1-3892) Qy | ORIGIN Alignment Scores: Pred. No.: Score: Score: Pred. No.: 1.64e-210 Percent Similarity: 87.87\$ Best Local Similarity: 87.87\$ Query Match: 96.44\$ Caps: C | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 167 Row: b Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF Location/Qualifiers 13892 /organism="Homo sapiens" /mol_type="mRNA" /clone="IMAGE:4375917" /tissue_type="Brain, hippocampus" /clone="Ibb="WIH MGC 95" /lab host="pH10E" /lab host="pH10E" /lab host="pH10E" /lab host="pH10E" | JOURNAL Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web Site: http://www-shgc.stanford.edu Contact: (Dickeon, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M. |
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| B & B & B & B & B & B & B & B & B & B & | D | DB Q2 DB Q3 DB Q3 | B & B & B & B & B & A | B Q B Q B Q B Q B |
| 359 ArgProProLeuGlnTrpArgTyrSerGluValSerPheMetGluLeuAspLysPheLeu 378 | ArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValHisSerLeu | 239 ABPGIYTHTALAVALABPILEPHASSTPHAGIYMETCYSALALAUGUMETALAVALLEU 258 | 159 SerAlaLeuSerPheLeuHisAlaCyeSerProProIleIleHisGlyAsnLeuThrSer 178 | 478 TTCATCACAGAGTACGTGTCATCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAGAAG 537 141 ABRHIBLYBALAMELABRALAAYG |

| RESULT 3 CQ729503 LOCTUS DEFINITION ACCESSION VERSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE AUTHORS TITLE JOURNAL FEATURES JOURNAL JOURNAL JOURNAL JO | |
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| CO729503 CO7 | 439 GluAspLysAlaArgTrpHisLeuThrLe 600 GAGGACAAGGCGCGCTGGCATCTCACTCT 459 GlnLeuThrTyrAspLeuLeuProThrAs 660 CAGCTGACCTACCTCTCCCCACCGA 479 HisTyrGlyPheLeuHisGluAspAspAr 479 HisTyrGlyPheLeuHisGluAspAspAr 670 CACTATGGCTTCCTCCACGAGGACGACCGACCGACGACGACGACGACGACGACG |
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| Clyser | Interest Interest |

| 140 LysasnhisLysalaMetasnalaargalaTrpLysargTrpCysThrGlnIleLeuSer | Qy 100 ProAsmIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCysAlaArgVal 119 | | 90.22% Indels: 6 Gaps: 7) x AX056416 (1-3304) UG1nValAsnGlnGlyAsnMetProGlyLeuG | ORIGIN ORIGIN ORIGIN Alignment Scoree: 2.3e-196 Pred. No.: 2.409.00 Percent Similarity: 98.72% Best Local Similarity: 98.29% Mismatches: ORIGIN Alignment Alignmen | AUTHORS Plowman, G.D., Martinez, R., Whyte, D. and Sudersanam, S. TITLE Protein kinases JOURNAL Patent: WO 0073469-A 60 07-DEC-2000; Sugen, Inc. (US) FEATURES Location/Qualifiers Bource /organism="Homo sapiens" /mol type="unassigned DNA" | - | Db 1369 GAAGACCGGCTGCACCGGCAGCTGACCTACGACCTCCCCAACCGACAGCGCCCAGGAC 1428 Qy 473 LeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAspArg 488 |
|--|---|--|--|--|---|---|--|
| Qy 500 LeuLysTyrArgGlyThrGlnAla 507 | 1243 CTGACCTACGACCTGCTCCCAACGGACGGCCCAGGACCTCGCCTCGGAGCTCCACCACGGACGG | Qy 420 ProPheAspSerGluThrArgClysVallleGlnMerGlnCysAsnLeuGluArgSerGlu 439 | Qy 380 AspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgProLeuGlyLeu 399 | Qy 340 GluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeuProArgProArgArg 359 | Qy 300 ArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValHisSerLeuLys 319 | Qy 260 IleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArgHisSer 279 | Qy 180 ThrilePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArgIlePhe 199 |

| US-10-618-9 Qy Db Qy Db | ORIGIN Alignment S pred. No.: Score: Percent Sim Best Local Query Match DB: | polyA_sign | gene CDS | FEATURES SOURCE | ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT |
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| 01974 (1-3538) | 8: ity: larity | /protein id="CAB70864. /db_xref="GI:6807783" /db_xref="GI:6807783" /db_xref="GI:670N250" /db_xref="Uniprot/Trem/ /db_xref="Uniprot/Trem/ /db_xref="Uniprot/TremAV /translation="MCALEMAV ARDPARRPSAHSLLFHKYLFEVI ARDPARRPSAHSLLFHKYLFEVI ARDPARRPSAHSLLFHKYLFEVI ARDPARRPSAHSLLFHKYLFEVI ARDPARRPSAHSLLFHKYLFEVI ARDPARRPSAHSLLFHKYLFEVI ARDPARRPSAHSLFHKYLFAM ARDPARRPSAHSH A | /dev_stage="adult" 13538 /gene="DKFZp434P086" /gene="DKFZp434P086" /gene="DKFZp434P086" /gene="bKFZp434P086" /pote="similarity to C.elegans H37N21.1/K10D3.5" /product="hypothetical protein" | This clone (DREZ#434P086) is available at the RZPD in Berlin. This clone (DREZ#434P086) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/. Location/Qualifiers 1. 3538 /organisme="Homo sapiens" /mol_type="mRNA" /db xref="caxon:9606" /clone="DKF2434P086" /tissue type="testis" /tissue type="testis" /clone_Tib="434 (synonym: htes3). Vector pSport1; host | |
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| 1003 CTCAÁGCTCCTGGCAGCCCACTGCTTCATCCAGCACCAGTACCTCATGCCTGAGAATGTG 1062 338 ValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeuProArgpro 357 | 278 HisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspPro 297 | 218 ArgAlaGluArgGluGuLeuArgAsnLeuHisPhePheProProGluTyrGlyGluVal 237 | 178 SerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArg 197 | 361 AGGACGGGGTTGGGGCAGCCTCGGGGACTGGGATGGTGAGGGGGTGCCCGGCCGCCTCGG 420 148 | 80 PheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuValAspHis 99 |

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Patent: US 6558903-A 9 06-MAY-2003;
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                                                                                                                                                                                                                                                                                                                                                  LeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThrSerAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                               PheIleThrGluTyrValSerSerGlySerLeuLy8GlnPheLeuLy8Ly8ThrLy8Ly8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGCGCACGAGGAGAAGATCCAGACCGTGTTCGAGCAGCTGGTGCTGGTGGACCACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuValAspHisPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGCGGCCCCGGAGCCGGCGCCGAGGCGGGCCCCGGGAACGGGAGCGGGAGCGGAGCGAC
                                                                                                                                    ACCGCTGTGGACATCTTCTTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATC
                                                                                                                                                                                     CGAGAGGAACTTCGGAACCTGCACTTCTTCCCCCCAGAGTATGGAGAGGTGGCCGATGGG
                                                                                                                                                                                                    ArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGluValAlaAspGly
                                                                                                                                                                                                                                                                                 ATCTTCATTCAGCACAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTCTCC
                                                                                                                                                                                                                                                                                                        IlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArgIlePheSer
                                                                                                                                                                                                                                                                                                                                                                                 AACCACAAGGCCATGAACGCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTCATC
                                     AGTGACCCCAACATGCGGGAGTTCATCCTTTGCTGCCTGGCCCGGGACCCTGCCCGNCGG
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Rarren, B., Linton, L., Nusbaum, C., Lander, E., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Changel, Y., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Good, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagod, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., LaRocque, K., Jones, C., Kanat, A., Karatas, A., Kalls, C., LaRocque, K., Jones, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McBean, P., McKernan, K., McPheeters, R., Meldrim, J., Norbb, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Politara, V., Nurbhy, T., Naylor, J., Naylor, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., Oliver, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stojanovic, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., M., Triyillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., M., Triyillo, J., Vassillev, H., Schauer, A. and Zody, M.
                                                                                                                                 CES 3 (bases 1 to 92291)

CES 3 (bases 1 to 92291)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, N., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Faro, S., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gadyna, S., Farorera, P., FitzGerald, M., Gage, D., Galagan, J., Gadyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., McCarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Mihova, T., Mabbitt, R., McCarthy, M., Macdonald, P., Major, J., Mihova, T., Mabhas, C., McCarthy, M., Macdonald, P., Major, J., Mihova, T., Mabhas, C., McCarthy, M., Macdonald, P., Major, J., Mihova, T., Mabhas, C., McCarthy, M., Macdonald, P., Major, J., Mihova, T., Mabhas, C., McCarthy, M., Macdonald, P., Major, J., Mihova, T., Mabhas, C., McCarthy, M., McCarthy, M., Phurkhang, P., Pierre, N., O'Neil, J., Nocol, R., Norbu, C., O'Connor, T., O'Donnell, P., Macdonald, R., Norbu, C., O'Connor, T., O'Donnell, P., Rachugha, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Tesfaye, S., Theodore, J., Topham, K., Stubbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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or accession nu
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Location/Qualifiers
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complement (4473. .4777)
/rpt family="Alu8x"
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complement (6348. .6820)
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complement(15346. .15495)
/rpt_family="MLT1C"
/rpt_family=100. .16464)
                                                                                                                                                                                                                                                                               complement (18519. .18684) /rpt_family="L2"
                                                                                                                                                                                                                                                                                                                     complement(17957. .18089)
/rpt_family="MER77"
                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="L2"
complement(17349. .17752)
                                                                                                                                                                                                                                                                                                                                                                                                                        complement (16869. .17347)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (16472.
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complement(14215...
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/rpt family="AluSq/x"
complement (13383..13736)
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/rpt_family="Aluy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (8785. .9 /rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="MER77"
17753. .17956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (12918.
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8208. .8505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="(CAAAA)n"
complement(7377. .7458
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7326. .7349
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|0615. .10690
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ement(16477
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ement(1201)
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                                                                                                                                                                                                             _family="GC_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             family="L2"
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Matches:
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| 286 | Qy 142 isLysAlaMetAsnAlaArg 148 Qy |
|--|--|
| 6 GGTCACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCCAACATGCGGGT | 20508 TCACAGAGTACGTGTCATCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAGAAGAAGAACC 20567 |
| 7 gValThrGluGluAlaileAlaArgAlaArgHlaSerLeUSerABpPrOAShmecArg- | 142 |
| CIGHCCICIOICAL TITLE INTERESTANTA TO THE TOTAL TO THE TOTAL TO THE TOTAL | 20507 |
| 0.0.0 to V COLDEN R CO. CO CO COLDEN REDEATOR OF COLDEN ROLL COLD ROLL C | 122 |
| ###################################### | Db 20388 CGCGAGGGTGAGCACGGGCAAGGCCCCGGGCAGGGCAGAGACCACAGCTAGGTGGGGCGGG 20447 |
| 1.4.6.6 こうごう でんさい こうさい こうさい こうじゅう こうしゅう こうしゅう こうしゅう こうじゅう こうしゅう こう こうしゅう こう こうしゅう こう こう こう こう こう こう こう こう こうしゅう こう | 118 |
| 21407 GGACATCTTCCCTTTGGGATGTGTGTGCGCTGGA-GGTACTGCCCCCCCCCC | Db 20328 GGTGGACCACCCGAACATCGTGAAGTTGCACAAGTACTGGCTGG |
| AspIlePheSerPheGlyMetCysAlaLeuGlu | 96 uValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCy 116 |
| CAGAGGTGGCCGATGGGACCGCTGT | CCCAGCGACCCTCCCTCCCCAGGAGAAGATCCAGACCGTGTTCGAGCAGCTGGTGCT 2 |
| 236GluValAlaAspGlyThrAlaVa 243 | 20208 |
| 7 CTTCCCCCCAGAGTATGGAGGTGAGTGGTGGTGCGGGTCCGGGGTGCCCACCCTGC | 82 AlaHisGlu 84 |
| 9 ePheProFroGluTyrGly | 20207 |
| 209 UPYOASDABDLEUNISSETPTOLLEARIA AGLINITUSTUSTUSTUSTUSTUSTISSETT 21286 | Qy 62 GluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLysAlaPheAla 81 Ph |
| GGGGGACGGGTCCTGGAGAGAGTCCCCGCCCGCTCAGCTCTTTTTTTT | CCCCAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATGGACACG 20147 |
| 203PeuArgProProThrAlaLe 209 | 45AsnGlnGlvAsnMet DroGlvJ.piiGlnSerThrDheT.piiAlaMet AsnThr |
| 21108 TTTCTCCCGCCCCTTGGCAGTGTGGCACCGAATCTTCTCCAATGG-TAAGTGCGGACTTT 21166 | く これしたようしょう てんせん ないない ないない ないない ないない はんしゅう しゅうしゅ ない こうしゅう はんしゅう はんしゅう しゅうしゅ しゅうしゅう はんしゅう しゅうしゅう しゅう |
| 194 ValTrpHisArgIlePheSerAsnAla 202 | 44 |
| 21048 GGGAAGGTGCCTGGAGCCAAGGGCAGAGGAGTTCTGATGCCCCCAGCAGCTAACTCCACTC 21107 | 199 |
| 3 | 44 |
| B GGCCTCATCAAGATCGGCTCCGGTGCTGGCGGGGGCAGGGCTGGGTGGG | 19908 CCCAGCCCTTGGATAGGAGCCCTTGGCTCCTGGGGGCAGCTACCCTCCAAGCCCCACCTT 19967 |
| 7 GlyLeuIleLysIleGlySer | 44 44 |
| B TGCAGCCCCCAATCCACGGGAACCTGACCAGCGACACCATCTTCATTCA | Db 19848 AGCCGCTAGCTTCCTGGGGATCCCCCTCGACCCCCTGAAACCTGCTCCAAATCCCCCTTAG 19907 |
| CABSELLO LIGHT HIR CANADA THE THE TRANSPORT OF THE TRANSP | Qy 44 44 44 |
| 8 AGULICIUM CUGGUICULUL INTELLITULUL INTELLITUL CUGANISTI INTELLITUL INTELLITULUL INTELLITUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITULUL INTELLITUL INTELLITULUL INTELLITU | Db 19788 CCCTGGGACTCCCTGAGGGCCAGTCTCCCCAGGACCACCTCCCCATGCCTCTGGACTC 19847 |
| | Qy 44 44 44 |
| B CGCTCAGGTGAGGGCCTGGGGCTGGGCGGCGCCACCCGAGCCCCCATCTCTCCAG | 19728 TCCGCGGCCCCTCGCGGCCCGAATCAGCCACCCCTGGACCCCTTTGGCCTGGCGCTCG 19787 |
| 0 | 44 44 |
| 8 CGACGGAGTCGTGCGTCCGCCGCCAGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCTG | 19668 GGGGCCTGGAGGCTGCGGGGGCGTGGGGGCCTGGGAGAGCGCGGCGGCTGGAAAACCTC |
| | 44 44 |
| B CTGGGCGAGGATGCGGGGCGGGCTCCGCAGGCCCAGCCGCCTCTCCTGCGCCCACCCGAC | 19609 CGGGAGCAGGT-GGGCGCGGGGGTTGGGGCACGGGGTGACACCCGCCCTCCCAGAGCGGGA |
| 148 148 | 41 AradludlaVAl |
| 20628 GGTTGGGGCAGCCTCGGGGACTGGGATGGTGAGGGGGTGCCCGGCGGCCTCGGACAGGGG 20687 | 21 GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg 40 |
| 148 148 | Db 19489 ATGGCGGCCCCGGAGCCCGAGGCGGGCCCCGGGAACGGGAGCGGGAGCGGGAGGA |
| | 1 MetAlaAlaProGluProAlaProArgArgAlaArgGluArgGluArgGluArgGluArgGluAsp 20 |

| Db | ş | ర్జ | ş | 문 : | 5 | B & | ? B | ঠ | ₽ | ঠ | В | ঠ | 망 | ş | 문 | ફ | 망 | ş | 당 | 8 | 망 | ş | 문 | ફ | 문 | ઇ | 밁 | ઠ | 당 | \$ | 밁 | ş | 망 | ş | 문 |
|---|------------|-----|------------|---|---|---|--|---|--|---------|--|---------|--|---------|--|--|---|-------------------------------|--|---|--|---|---|---------|--|--|--|---|--|-------------------|--|---|---|--|--|
| TGGCTGGGGAGGTTGGGACGTGGAAGGGGCCCTGCAGGACCCACGGCCTGAGCA | 329 329 | | 329 | CGGCCCTCTGCACGACGCCTCTCTTCCACCGCTGCTCTTCGAGGTGCACTCGCTGAA | 299 GATGDTGSerAlaHigSerI.eniDebeHigaYrValionDbeClinValVieSerIeniTv 21 | 20/ | CTCAGGGGCCACCTCTCCTCGAACTGCGGGGCCAGAGCAGAGAGCCCTTGCACACCACCA | 286 | 22426 GACTCCTCCCTATGGGCATCCCTGCATGTCCTGTGTGTCCCTGAGGAGGGACATGGGGAA 22485 | 286 286 | 22366 CCAGAACCCAGCTGTCCTCAAGCTCAGAGGACCAGGTCCTGGCCTGGCTGCTGCTGCTGG 22425 | 286 286 | 22306 TCATGGCTTCTCCCCACGATTTTTTGGGGGTCGAGGGAAGCAGAGCATGGTGCTCCAATC 22365 | 286 286 | 22246 GGCCCGAGCTGAGCCGATCAAAAGGCCATGGGTAGGAGGCTTGCAGGTGTGACTTTAGGA 22305 | 286 286 | 22186 AGCCGGGCTGGGCACGGATGTGGACAGAGTGGGGGACCCATCAAGGTCGTCTCCAGTGTTG 22245 | 286 286 | 22126 AGACTTAACTCCATGGCCTCAGGAGATGGGGGGTGCCTGGTCGGGGGCTGGTGGCGAGCTGG 22185 | 286 286 | 22066 AGCAGGCAAAAAGAGGTATGGGATGGAAGCTGCATCCACAGCCCCCTCTGCTCGGAGTCT 22125 | 286 286 | 22006 GACTTTAAGCTTCCAGGAGGTGATGAGGCTCCAGCTTGTGGGGGGGACATGGTGGGTG | 286 286 | 21946 GCTTTAGAGTGAGTGGTGGAGCCAACATCTGCACCTGGGTCTGCTTCACTCCAAGTCCTT 22005 | 286 286 | 21886 ATCACCATGCCCGTTTTATAAAGAAACCAAGGTTCAGAGGAGATGAGTCCTTTGCCCAAG 21945 | 286 286 | 21826 TAAGGGGTCAGCACATTCTAAGGACAAGAAGGCAAGAGAGACCCTCCCT | 286 286 | 21766 TGCACCCCTCCCAAAGAGGACCTCAGTGGGAGCACATACTGGTTCCAGGCCTGAAGGCCC 21825 | 286 286 | 21706 GCTCCAGGCAGACCTGGGAGAACATCACAGTTTGTGCAGTTGAGGGGGTATACCAGCTGAC 21765 | 286 | 21646 AAGCAGCTTGCCCTGCCCCCAGCTGGCTCACCGTGCTCAGCTAGGGCTAGCAAGGT 21705 |
| Db 23802 GTCCTCAGCTGACGCCCAGGCTCTGGGAGGCCTGATCCCGCAGGCACCGTGCACTTCGGC 23861 | Qy 428 428 | 23 | Qy 428 428 | Db 23682 CCCCAGACTTTTCCTGCAGCACCCCCTCCTGGCCAGGGGCCTCTCTCGGTGCAGTGCAGC 23741 | Oy 428 428 | Db 23622 CCCCCACCCTCCCATCCCCACCTGGTGCTGATTCCCGGACATCTATGTCCTGGTGTCT 23681 | 428 | 23562 CACCCGGGCTCTTCCACCCTGCCAGCAATCTTCCCCCACCCCCGCACCCCTCCCACCCC | OV 428 | 200 | 23 | 428 | 23 | 428 | 23 | 2- | 23283 CITTGACTCTGAGACCAGAAAGGT-GAGTCCCCTCTCCTGCTGCTCAGTGCCATCCCTCA | 420 opneAspSerGluThrArgLysVal | 23203 CCGTGTGCTGGCCCCACCCCCGAGGAGGTCCAAAAAGGCCAAGACCCCGACGCCAGAGCC | 400 oArgValieuAlaProProGluGluValGlnLysAlaLysThrProThrProGluPr | 23143 CCCCAGGAATCGAATCTACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCC | 382ArgAsnG1y11eTyrProLeuWetAsnPheAlaAlaThrArgProLeuG1yLeuPr | 23083 TGATGTAAGGTTGGGGGCAGGCAGCTGTCAGGCCTGAACCCCCAGCCACCCTGTTGTGT | | 23024 GTACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGT-CAGGTGAGAAC | 366 - TyrserGluValSerPheWetGluLeuAspLysPheLeuGluAspVal | 22964 C | Grant Control of the | zz905 GCTGCAGTGGCG-GTGAGCAGTCAGCACCCAGAAGCCTCCCCCACACATCCCCTCC | 361 OLEUGINTTDATG | 22845 GACCAAGGCCATGGACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGCAGGCCCCC | 341 8/17/14/8A.AMECASDLEUH1SA.LAVALLEUALAGLULEUPTOARGPTOARGARGPROPT | 22786 CACCGCCTTGATGCTCTTGTGGCCGCAGAC-CTCATGCCTGAGAATGTGGTGGAGGAGAA | 330GlnTyrLeuWetProGluAsnValValGluGluLy | |

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                                                           REFERENCE
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                                                                                                                                                                             KEYWORDS
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                         AUTHORS
TITLE
                                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                       24641 AGTACCGTGGGACCCAGGCC 24660
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                                                                                                                                                                                                                                                                                                                                                                                                                             24581 CCCTCCTTCCGCAGGACGACCGGATGAAGCTGGCCGCCTTCCTGGAGAGCACCTTCCTCA 24640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24521
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Mus musculus chromosome 15 clone RP23-42819 map
IN PROGRESS ***.

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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (house mouse)
                   1 (bases 1 to 174949)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 15, clone R
                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea, Muridae; Murinae; Mus.

1 (bases 1 to 174949)
                                                                                                                                                                                                                                                                                                                                                                                 YSTYrArgGlYThrGlnAla 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------LeuThrLeuLeuLeuValLeuGluAspArgLeuHisArgGlnLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCTGCCGTGGGGAAGGCGGGAGCGTGGCGGAGCCCTGAACCCCCAGCCGACCACGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCATGTGAGCGGGGCCTGGGAAGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTGCTGCTGGGTTTGTGAGTCCCAGCCTTCCCCCGCTGCAGGTCATCCAGATGCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTCTCCCGCGGTGAAAGCTCCTATTCAGCCTTCAGTACCCAGCCCCTAATGTCGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGACCTCGCCTCGGAGCTCGTGCACTATGGCTTCCTCCACGA-GGTGCGCTGGGCGGCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGlu--------
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                                                                                                                                                                                                                                                       musculus chromosome 15 clone RP23-42819 map 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspAspArgMetLysLeuAlaAlaPheLeuGluSerThrPheLeuL
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                       RP23-42819
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NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                             Center: Broad Institute of MIT and Center code: WIBR
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                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farcara, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Ntcol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Fhunkhang, P., Pierre, N., Pollara, V., Royanan, C., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Sto'Janovic, N., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Sto'Janovic, N., Viel, R., Voa, Mark, 2002, Whitched (Jan, N., Ve, W.J., Young, G., Direct Submission) Whitched (Jan, Marc, A., and Zody, M. CE 3 (bases 1 to 17449)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, M., Barna, N., Bartien, V., Anderson, M., Anderson, M., Barna, N., Bastien, V., Anderson, M., Anderson, M., Bastien, V., Bloom, T., Boyuslavkiy, L., Boukhgalter, B., Conkarata, J., Chang, J., Cheopel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Brickson, J., Faro, S., Graham, L., Grand-Pierre, N., Hafez, N., Erickson, J., Faro, S., Graham, L., Grand-Pierre, N., Hafez, N., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Galagan, J., Gardyna, S., Graham, L., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Seoman, S., Severy, P., Smith, C., Spencer, B., Schupback, R., Seoman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teafaye, S., Theodore, J., Topham, K., Milson, B., Wi, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Shbmitsolon
Direct Submission Submitted (02-AUG-2005) Broad Institute of MIT and Harvard Charles Street, Cambridge, MA 02141, USA
On Aug 2, 2005 this sequence version replaced gi:71067273.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) Submitted (28-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA http://ftp.genome.washington.edu/RM/RepeatMasker.html and Harvard,

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| 8591uLysileGlnThrVal 90 | 74 PheGlyAspArgLysAlaPheAlaAlaHisGlu | 54 SerThrPheLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHis 73 | 45 | 5959 AGCACATTCACGGCTGGGGGAAGGTTGTGGCGGGAGACCACGTCCACACCCTGGGTCTATT 6018 | TGGGTTCTTGATTCCCAGCCTTACCTCCTCAGCCCTCCCACTGAGCTGGGCAAGGCTAGC | 5839 CCCAACCTCTAAAACCTGCGTACCTTCTGGCCCAGCCCCTGGACACCCACC | 44 44 | 44 44 5779 TGTCATACTGGGACCACCTCCACGTGCCTCTTGGATCCCTACTACCGCTCTGGGGATCTC 5838 | 5719 GGCCCTCGGATCCCTTTGGCCCCAAGCCCCTGGTGAGAAACCCCCCATTCCTTGAACACCGG 5778 | | CCATGGGATCCGTGGGGCCGAGCCAGTATGAGGGTCTCCCCGGACGCCCTGGCCTCTGGA | 44 44 | 41 ArgGluGlnVal 44 5600 CGGGAGCAGGT-GGGCACGGGTGACGCCGCCGCCGTCCCGTAGCCTAAGGATAGAAG 5658 | 5540 GAGAGCGAGAGCGACATCCTGGAGGAGAGCCCGTGTGGCCGCTGGCAGAAGCGG 5599 | 21 GluserGluAspGluserAspIleLeuGluGluserProCysGlyArgTrpGlnLysArg 40 | 1 MetAlaAlaProGluProAlaProArgArgAlaArgGluArgGluArgGluArgGluAsp 20 | 618-941-99 (1-507) x AC116487 (1-174949) | 58.56% Indels: 14 Gaps: | | ent Scores: | | /db_xref="taxon:10090" /chromosome="15" /map="15" | /mol type="genomic DNA" | t Loc |
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| 7277 AGAACTGACCAACGCTGTCTTGCTTCTCCCATTTCAGAAGTCAATGATGGGACTGCTGTG 7336 | | 11 Spaspiewargaeirroliekargalasiwargstusidinargasniemiishepher | 97 GTGTGGGGACCATGGAGAAACTTGTCTGTTTAGCCTCCACCCTTTTCCTCAGCACTTCCTG | ::: | 6977 GGGAGCCCTGGACAGAGACTGCCCAGTCTCCCCGCCCAACTGACATCCTGTCTTTCTCTC 7036 194 | | 190 sIleGlySer | 1/9 Oletlenessymmetrinzserasyntriephelleginhiskengiyleuilely 190 | 97 CCGGTTCTTCCTGCCTCTCATCCTCTATGCTTTGCAGCTCTTTTGCACGCCTGCAGTCCCCC | 162 SerPheLeuHisAlaCysSerProPr 170 | 6737 AGAGCCTGGCCTTGCCCACGCGCTTGCCCCCTGCTCTGCACCTTTCCGCTGCTCTCTGAC 6796 | 161 161 | GIGCGTCCGCTGCCAGGCCTGAAGCGCTGGTGTACGCAGATCCTGTCTGCACTCAGGTG | 6617 GTGGGGTAGCGGGCGCGCAGGCTCCAGCAGGCTTTTGGTGCCCACCCGACGCAGTC 6676 | | GTCCAGCAGAACTTAGGGACAGTAGTGGGGGGGGGGGGG | 6497 AAGAAGAACCACAAGGCCATGAACGCCCGGGTATGGGGAGTGGGCTGGGGGACTGGAGGGA 6556 | 39 LysLysAsnHisLysAlaMetAsnAla | 119 ValllePheIleThrGluTyrValSerSerGlySerLeuLyBGlnPheLeuLyBLy8fhr 138 | 6377 ACAGGCTGGGTGGGGCAGCATGGAGACCCACCCGCAACGGCGGAGCCCGGCTGCCCGCAG 6436 | 16 | 111 AspThrSerGluAla 115 | 6258 TTTGAGCAGCTGGCGCTGGTGGACCATCCCCAACATCGTCAAGCTGCACAAGTATTGGCTG 6317 | 91 PheGluGlnLeuValLeuValAspHisProAsnIleValLysLeuHisLysTyrTrpLeu 110 |

| Qy 446LeuThrLeuL 449 | 366TyrSerGluValSerPheMetGluLeuAspLysPheLeuGluAspVal 381 | , Š. Š. |
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| QY 437 rgsergluasplysalaargitphis | 365 365 | } |
| 9373 CTCTGTGGCTAATACACCTTCCCTGCCCACAGGTGGTCCAGATGCAGTGCAACCTGGAAA | 354 euProArgProArgArgProProLeuGlnTrpArg | B 8 |
| Db 9313 GAGACCATTTACCATCTTTGGGTCTCTGCTGCTCCTTCTGGGCTCCTCTGTAAAGCCGTG 9372 | 36 CTGAGAATGTGGTAGAGGAAAAAGACCAAGGCCATGGACCTCCATGCAGTTTTGGCTGAGA 82 | B 2 |
| 429 | 8176 GCAGGACCCTTAGGTTGGGTCCATCCCCATGAGCACTTGTGTCGTTCACAGACCTCATGC 8235 | § B |
| Qy 429 429 Db 9253 TGGAAGCTTCCCTAATACTCAGGGCTGGTGCAGTAAGACGTGCTTTTCCGACTTCCCTTG 9312 | 332LeuMetP 334 | Qy |
| 9193 CTCCCCCATCCCCTCTCTGGCATTGTATTCATCATTCAGGACCCAAACCGAAGGCTGTCT | 331 yr 331 8116 TGAGGGGCAGAAGGGCCGGGGTGGGTCAGGATCCTGGGGTCAGGTAGTGGAAGGGTCTTT 8175 | 음 5 |
| Db 9133 CCTGCGGGGCACAGCGTTTCTTTGCTTTCCACGGTTCTCTGTTTCTGTCTCTCTC | GCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTTCATCCAGCACCAGTG | dg d |
| Qy 429 429 | . 311 | 8 8 |
| CCTAAGCCCCAGCCTCCTGCTCCTCCTGGTGGCACCTTGGTTTTCTGTACAGTCACAC | 291. sCysLeuAlaArgAspProAlaArgArgProSerAlaHisSerLeuLeuPheHisArgVa 311 | ş |
| Db 9013 CACCCTAAATTCAATTGCCAGTAGTCTACATGGCCTGCCCAGAGAACTAGTGGAAATCAG 9072 | 7936 CGAGGACTTTTCCAGCTATCACCTGTCTTTCTTGTTTACAACCTAGGAATTCATCCTCTC 7995 | B |
| 429 | 287GlupheIleLeuCy 291 | § |
| Db 8953 GTCTGGATCCAGAGCCATTGCTCCGGTCTCCCTTCTCATAGCTTCCTTC | 7876 GTGGGAGGATGTGGTGATTGGACCGGTGGGGTCTAGAGTCTTGAAGGACCTCCTCTAGAG 79 | 문 4 |
| Qy 429 429 | 7816 CIGCTAAIGGGAIGACTICTCIGCTCATTCATACAGGAAGGCTCTTTCAGCATCCCTGAG 7 | ? B |
| 8893 AGTCCTTCCCCCATCCGGTTGCATGCTCTCTTCCAGAGGCTTTGGCTACGTCTGTTCCCC | 286 286 | : হ |
| Oy 429 | 7756 GCATACGTGTTTGGAGCCCAAGGCTTGCCTGTCCTCAAGTGTCCAGAATCAGATCTTGAG 7 | 뫄 |
| 429 | 286 | Ş |
| Db 8773 CCCGCCTCTCCCCATCCCCGTTCTCCCCCAGGCTGCCAGAGACCAAATCCAAGCTGACCC 8832 | 7696 CCACCTGAAAGGAAGACTCTTCCAGAAGCTCCACAGACTCCACAAGGGTGAATGGAAGTAG 7755 | 문 |
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| Db 8713 GTGCTGTCTCTAGGAGTTGACCACAATCAGGGAATGGAAATGGATGCCTTTCTCTGGGGA 8772 | 7616 GTD & & PTOTA DAG BACK CONTROL TO THE ACT OF THE AC | 3 S |
| 429 | 7576 TGCAGGTGCTTCAGCTTACCCTTGAAGTGCTCTAGGCAGGC | , B |
| Qy 416 roThrProGluProPhahapserGluThrArghysValIle | 286 286 | Ş |
| 8594 CCTTGGGGCTTCCCCGTGTGTTGGCCCCACCCCCAGAGGAAAGCCCAAAAAGGCCAAAACTC | 278 HisSerLeuSerAspProAsnMetArg | B & |
| Db 8534 CCCCCTTGTCTATCCCCAGGAACGGGATCTATCCACTGATGAACTTTGCGGCTGCTCGGC 8593 Ov 396 roLeuGlyLeuProArgValLeuAlaProProProGluGluValGlnLvsAlaLvsThrP 416 | 7456 CTCGAGATCCAAGCCAACGGGATACCAGAGTCACAGAAGAGGCCATCGCTCGAG | 망 |
| 382ArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgP | 258 LeuGluIleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAlaArgAlaArg 277 | ₹ |
| 8474 GAGCTGGCATGAGACTGAAGAAAAAGCACTATCAGGCCTGAGCCCCACCTAGCTACCCA | 255Metalaval 257 256 TGCTCCAGGGTCTACGCCATCCCACCCAATTCCCAATTTGTCCCTGCACCCAGATGGCTGTA 7455 | B & |
| Db 8415 CTAGGTACTCAGAGGTCTCCTTCTTGGAGCTGGACAAATTCCTAGAGGATGT-CAGGTGA 8473 | 244 AspIlePheSerPheGlyMetCysAlaLeuGlu | Qy Oy |

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Submitted (10-FEB-2002) Whitehead Institute/MIT Center for Genom Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 202844)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Anderson,S., Arachchi,H.M., Barra,N., Bastien,V., Bloom,T., Boguslavkly,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
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Birren,B., Nusbaum,C. and Lander,E.
Musumusculus chromosome 15, clone RP23-192B21
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AC110211.16 GI:55416090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGCTGCCCGGTACTACCATGCTTCCCTACTCATCCACTGCAGGATGACAGGACAAAGC 9850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCCAAG-TAGG 9611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euLeuValLeuGluAspArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThr----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCAAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 202844)
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RP23-192B21, com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (05-NOV-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 5, 2004 this sequence version replaced gi:53793775.
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Submitted (05-OCT-2004) Whitehead Institute/MIT Center for Genome Submitted, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: L20862
Center clone name: 192_B_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                    20570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21043 ATGGCGGCCCGGAGCCGGCGAGGAGAGGC-----CGGGAGCGCGAGCGGAGGAC
                                                                                                                                                                                                                                                                                                                            20630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetAlaAlaProGluProAlaProArgArgAlaArgGluArgGluArgGluArgGluAsp
                                                                                                                                                                  SerThrPheLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHis 73
                                                                                                                                                                                                                                                                                                                                                                                     CCCAACCTCTAAAACCTGCGTACCTTCTGGCCCAGCCCCTGGACACCACCCTTCTCCCCC 20631
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32.50%
31.69%
58.56%
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Matches:
Conservative:
Mismatches:
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12
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984
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|--|-------|-----------------------------------|--|--|---|--|---|--|---|--|-----|---|--|---|--------|------------------------------------|--|----------|--|--|
| Qy 366TyrserGluValSerPheMetGluLeuAspLysBheLeuGluAspVal 381 | 18174 | Qy 354 euProArgProProLeuGlnTrpArg | 394 rodinasnyalvalgingintysthrtysalamechapteuHisalaValteuAlaGlut | 18353 GCAGGACCCTTAGGTTGGGTCCCCATGAGCACTTGTGTCGTTCACAGACCTCATGC | 18413 TGAGGGCAGAAGGGCCGGGGTGGGTCAGGATCCTGGGGTCAGGTAGTGGAAGGGTCTTT | 111 LEGITIES UN GAIRLES SE LEGIUS BIEGLEGIA AGAIRLES Y PERELLEGIANA BGID - I | 291 BCYSLEUK.AARTGASPFTOA.IAARTGASPFTOSERALAHISSETLEULEUPHEHISARTYA | 18593 CGAGGACTITTCCAGCTATCACCTGTCTTTCTTGTTTACAACCTAGGAATTCATCCTCTC | 18653 GTGGGAGGATGTGGTGATTGGACCGGTGGGGTCTAGAGTCTTGAAAGGACCTCCTCTAGAG | Qy 286 286 | 286 | Db 18773 GCATACGTGTTTGGAGCCCAAGGCTTGCCTGTCCTCAAGTGTCCAGAATCAGATCTTGAG 18714 | 18833 CCACCTGAAAGGAAGACTCTTCCAGAAGCTCACAGACTCCACAAGGGTGAATGGAAGTAG | 286 | Qy 286 | 18953 | Qy 278 HISSETLEUSERASpETOABRMELATG | 19073 (7 | 19133 TGCTCCAGGGTCTACGCCATCCCACCAATTCCAATTTGTCCCTGCACCCAGATGGCTGTA | Db 19192 GACATCTTCTCCTTCGGGATGTGTGCACTGGA-GGTACTGTCCACTCTCCTCATAGCCCC 19134 Qy 255MetAlaVal 257 |

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| 430GlnMetGlnCysAsnLeuGluA 437 17156 CTCTGTGGCTAATACACCTTCCCTGCCCACAGGTGGTCCAGATGCAGTGCAACCTGGAAA 17097 437 rgSerGluAspLysAlaArgTrpHis | 17336 CICCCUAICCCICICINGCAITGIAITCAICAITCAIGACCCAAACCGAAGGGIGICI 17277 429 | CCTAAGCCCCAGCCTCCTGTCCTCCTCCTGGTGGCACCTTGGTTTTCTGTACAGTCACAC CCTGCGGGGCACAGCGTTTCTTTGCTTTCCACGGTTCTCTTTCTGTTTCTGTCTCTCTC | 17576 GTCTGGATCCAGAGCCATTGCTCCGGTCTCCCTTCTCATAGCTTCCTTC | CCCGCCTCTCCCCATCCCCGTTCTCCCCCAGGCTGCCAGAGACCAAATCCAAGCTGACCC CTTTGTGGAAGCTGGAACCGGACCGACACAATCATTTCCCCCAGAGGCTTCTTGCTTTTAC AGTCCTTCCCCCATCCGGTTGCATGCTCTCTTCCAGAGGCTTTGGCTACGTCTGTTCCCCC | 381 |
|---|---|--|---|--|---|
| | AUTHORS Han, J., Montgomery K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R. TITLE Direct Submission Submitted (11-SEP-2002) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA COMMENT On Sep 11, 2002 this sequence version replaced gi:18071317. | 2 (bas Han, J., Ioshikh Gordon, Direct Submitt Einstei Bronx, | ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutharia; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 213817) AUTHORS Han,J., Montgomery,K.T., Grills,G., Lee,E., Long,J., Pomerantz,R., Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A., Gordon,M., Goltz,J.S. and Kucherlapati,R. TITLE High Throughput Mouse Sequencing JOURNAL Unpublished | ACCESSION ACOS1615 ACCESSION ACOS1615 ACCESSION ACOS1615 ACCESSION ACOS1615 ACCESSION ACOS1615 ACCESSION ACOS1615 ACCESSION AC | 449 euLeu 16976 TCTTG 467 16917 CTGGT 468 16857 TGTCC 480 YrGly 16797 ATGGC 486 16738 CGAGC |

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Quality coverage: agarose-FP - N/A
Quality coverage: 6.8 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 **Estimated insert size: 212917 - sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is
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   201069
201766
201786
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137 213256: gap of unknown length
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                                                                                                                                                                                                         note="assembly_name:Contig196"
                                                                                                                                                                                                                                                                                                                      estimated length=unknown 17213. 133385
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205759:
205779:
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11570: gap of t
112106: contig c
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212126: gap of t
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                                                                                                                                                         y_name:Contig195"
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ig of 328 bp in length
of unknown length
ig of 269 bp in length
of unknown length
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g of 507 bp in length
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of 1042 bp in length
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of 405 bp in length
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of 260 bp in length
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of 511 bp in length
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of 174 bp in length
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of 374 bp in length
unknown length
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| Qy 74 PheGlyAspArgLysAlaPheAlaAlaHisGlu | Oy 54 SerThrPheLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHis 73 | Qy 45 | OY 44 44 Db 13331 AGCACATTCACGGCTGGGGGAAGGTTGTGGCGGAGACCACGTCCACACCCTGGGTCTATT 13390 | QY 44 44 Db · 13271 TGGGTTCTTGATTCCCAGCCTTACCTCCTCAGCCCTCCCACTGAGCTGGGCAAGGCTAGC 13330 | QY 44 44 Db 13211 CCCAACCTCTAAAACCTGCGTACCTTCTGGCCCAGCCCCTGGACACCACCCTTCTCCCCC 13270 | 13151 TGTCATACTGGGACCACCTCCACGTGCCTCTTGGATCCCTACTACCGCTCTGGGGATCTC | Db 13091 GGCCTCCGGATCCCTTTGGCCCCCAAGCCCCTGGTGAGAAACCCCCATTCCTTGAACACCGG 13150 Oy 44 | Qy 44 44 | Qy 44 44 Db 13031 CCATGGGATCCGTGGGGCCGAGCCAGTATGAGGGTCTCCCCGGACGCCCTGGCCTCTGGA 13090 | Qy 41 ArgGluGlnVal44 Db 12972 CGGGAGCAGGT-GGGCACGGGTGCGGGTGCCCGTAGCCTAAGGATAGAAG 13030 | Qy 21 GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg 40 | Qy 1 MetAlaAlaProGluProAlaProArgAlaArgGluArgGluArgGluArgGluAsp 20 | US-10-618-941-99 (1-507) x AC051615 (1-213817) | Percent Similarity: 32.50% Conservative: 12 Best Local Similarity: 31.69% Mismatches: 24 Query Match: 58.56% Indels: 984 DB: 14 Gaps: 19 | Length: | sc_feature | /estimated_length=unknown misc_feature 178793181465 /note="assembly_name:Contig190" gap 181466181485 |
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| 449 euLeuValLeuGluAspArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThr 467 | 381 |
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| 446LeuThrLeuL 449 | ⊢ ພ |
| 13/ FGSETGILMSDIVSALEARGITCHIS | QY 365 365 Db 15727 CCTTCCTAGCTGCTTGGCCTTGCCCTGACATCTCTCATGTACCTTCCACACCATT 15786 Db |
| OGlimetGlicysAsnieuGlia 5 CTCTGTGGCTAATACACCTTCCCTGCCCACAGGTGGTCCAGATGCAGTGCAACCTGGAAA | OY 354 euProArgProArgProProLeuGlnTrpArg |
| 9 GAGACCATTTACCATCTTTGGGTCTCTGCTGCTCCTTCTGGGCTCCTCTGTAAAGCCGTG | Oy 334 rogluaenValValgluGluLyeThrLyeAlaMetAepLeuHisAlaValLeuAlaGluL 354 |
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| | Qy 258 LeuGluIleGlnThrAsnGlyAspThrArgValThrGluGluAlaileAlaArgAlaArg 277 |
| 46 GAGCTGGCATGAGACTGAAGAAAAAGCACTATCAGGCCTGAGCCCCACCTAGCTACCCA | QY 255 |

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DEFINITION
ACCESSION
VERSION
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Allen, C., Allen, H., Abbrooks, S., Amin, A., Angulano, D., Ander, J., Angulano, D., Anyajabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Catter, K., Cavazos, I., Ceasar, H., Center, A., Chen, C., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Checko, J., Chen, S., Davy, Carroll, L., De Anda, C., Dederich, D., Devis, G., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falla, T., Fan, G., Palla, T., Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17104 ATGGCTTCCTGCACGA-GGTGGGCGGGTGCGCTTTGGGTGTGGAAAGGTGCAGGGTCTGC 17162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17044 TGTCCTGTGTTCTCTCTCAGCGGACAGTGCCCAGGACCTCGCTGCAGCTAGTGCATT 17103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491
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AC132640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muzny, D. Marie., Metzker, M. Lee., Abramzon, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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norvegicus clone CH230-339B14, WORKING
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced g1:23908481.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Williams, G., Wilson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 194709)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (02-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 194709)
Rat Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                          shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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    Genome Center
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REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE JOURNAL

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Center project name: KBQF

Center clone name: CH220-339B14

Center clone name: CH220-339B14

Center clone name: CH220-339B14

Assembly program: Phrap; version 0.990329

Consensus quality: 188047 bases at least Q40

Consensus quality: 189447 bases at least Q20

Consensus quality: 199412 bases at least Q20

Betimated insert size: 195068; sum-of-contigs estimation Quality coverage: 8x in Q20 bases; sum-of-contigs estimation Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM Project Information

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.

This sequence will be replaced

by the finished sequence as soon as it is available and the accession number will be preserved.

1 194709: contig of 194709 bp in length.
Location/Qualifiers

1. .194709

FEATURES

/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116" /clone="CH230-339B14"

misc_feature

| 8 | 문 왕 | р 9 | g 49 | ₽ : | & B | ş | B 8 | 당 5 | ? ₽ | 8 | В | ş | Db . | ş | <u> </u> | g | ફ | US-10- | Query I | Score: Score: Percent | Alignm | ORIGIN | я | | mí | |
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| n 88 | 72 LeuHisPheGlyAspArgLysAlsPheAlsAlaHisGlu | 52 LeuGlnSerThrPheLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGlu 71 ::: | 45 | GCTAGCAACACTTCATGGCTGGGGAAAGGTTGTGGCAGAGACCACGTCCACACCCTGGG 54823 | 54942 CCCCTGGGTCATAGATTCCCCAGCCTTACCTTCCCCAGCTTTCCCCAGCTGAGTTGGGCAGG 54883 | - 44 | 44 44 55002 TCCCCAACCTCTAAAACCTGCTTTACCTTCTGGCCCAGCCCCTGGACACCCACC | 55062 TGTCATCCCGGGACCACATCCACGTGCCTCTTGGATGCCCCCACTACCCCCTCTGGGTATAG 55003 | 2 GGCCTCGGATCCCTTTGGCCCCAAGCCCTGGTGAGAAACCCCCCAAACCTTGAACACCAG 55063 | 44 44 | 55182 CCATGGCATCCGAGAGGCCGAGCCAGTATGAGGGTCTCCCCCGGACGCTCTGGCCTCTGGA 55123 | 44 | | 41 ArgGluGlnVal 44 | 21 GlusergluagpGluserAspIleLeuGluGluserProCysGlyArgTrpGlnLysArg 40 | 55355 ATGGCGGCCCGGAGCCGGCGCCGAGGAGAGGCCGGGAACGCGAGCGGGAGGAC 55302 | | 7) x AC132640 (1-194709) | 58.26% Indels: | 7.18e-121 Length: 1555.50 Matches: 31.32% Conservati | | end_sequence:BZ164293" | nisc_feature complement(191365192203) /note="clone_boundary clone_end:Sp6 fite: | <pre>clone_end:T7 site: end sequence:BZ16</pre> | <pre>8c_feature 7050. 79 /note="cl</pre> | /nore="wgs_end_extension clone_end:T7"extension |
| Qy 236GluvalAlaAspGl 240 | Qy 228 HisPhePheProProGluTyrGly 235 | Db 53684 GCACTTCCTGACGATCTCCGGAGCCCTATAAGAACTGAACCGGAGGAGCTCCGGAAACCTG 53625 | 53744 GGTCTCTGGGGTGTGGGAGCTGTGGAGAACTGGTCTGCTCAGCATCACACTTTTTCTTA | 53804 CTCTTTCTCTGCGTCGGCCGTTGCAGTGTGGTACCGCATC | 194ValTrpHisArgIlePheSerAsn | Qy 193 | Db 53924 ATGGCCTCATCAAGATCGGCTCTGGTGCTGGCGAGGGGGGGG | 53984 CCTGCAGTCCCCCCATCATCCACGGAAACCTGACCAGCGACACGATCTTCATTCA | 166 laCysSerProProIleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisA | Qy 161 | 54104 CAGGTGAGAGCCTGGCCTGCCCACGCACTTGCCCCCTGCTCTTCCTTTCACCTTTCTTT | Oy 160 160 | 54164 GGAGTCGTGCGTCCGCTGCCAG | Qy 149AlaTrpLysArgTrpCysThrGlnIleLeuSerAla 160 | 54224 TCAGGAGTGGGGTAGCGGGCGGGCTCCGCAGGCTCAGCAGCCTCTTGGTGCCCACCCGAC | Db 54284 GAGGGAGTCCAGCAGAACTTAGGGACAGTAGTGGGGCGGGGGACTCCGAGAGGCCTCGGT 54225 | Qy 148 148 | Db 54344 AAGACCAAGAAGCACAAGGCCATGAACGCCCGGGTATGGGGAGTGGGTTGGGGACTG 54285 | Oy 137 LysThrLysLysAsnHisLysAlaMetAsnAlaArg 148 | Oy 117 AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLy8GlnPheLeuLy8 136 ::: | Db 54464 GAAGCCACAGGCTGGGTGGGGCAGCATGGGGAACCCACCC | Oy 116Cys 116 | Qy 109 TrpLeuAspThrSerGluAla 115 | ::: | 68 | D) \$4644 TTTTGCCCTTATATACCCTTCATTCCCCCCCCCCTTTCTTCTTCT |

| .86 GGCTAGGCTTIGGCTTGATGCCTCTTATGTCTTATGACACCTCTTCCATACCATCCCAGG 52 | 65 | | 150 Arg DroProTenic 1977 1 | 339 SINGANANGACCANGGACCTTCANGCAGTGTTTGCCTTGAGATGTCCCAGTCCCATT 52546 2605 GAGGAAAAGACCANGGACCTTCANGCAGTGTTTGCCTTGAGATGTCCCCAGTCCCATT 52546 | [] : [] : [] : [] : [] : [] : [] : [] : | 55 TTGGGTCCATCCCATGGGCATTTCTGTGGTTCACAGACCTCATGCCTGAGAATCTGGTA 5 | 2LeuMetProGluAsnValVal 3 | 25 GCCGGGGTGGACCAGGATCCTGGGGTCAGATCATGGAAGGGTCTTTGCAGGACCCTTAGG 5 | | 316 1856ETHOUNGHOADAGAANAANAANAANAANAANAANAANAANAANAANAANAA | S ACCCIGCCGACCCICAGCCCACAACCICCICTTCCACCGAGIGCTCTTTGAGGIGC | SpProAlaArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValH 3 | accuaciace Treffeceda accuragan rearce references accuration and the second accuracy | GlupheIleLeuCysCysLeuAlaArgA 296 | | 286 286 | 5 AATGGGATGCCTTCTCAGGCAGGCATGATGGAGGACATCATTGTGGAGGTGGGAGGATGC 5 | თ | S GGTGTTTGGAGCCCAAGGCCTTCCTGCCCTCAAGTTTACAGAATCAGATCCTGAGCTGCT 5 | 286 | AAAGGAAGACTCTTCTAGGAGCTCACGGAATTTCAAGAGGGTGAATGGAAGTAGGGCATG S | 286 | 3205 GGTCAGTACATTTGAAAGTGTTAGCATCTGAAAGCGTAGCTGGCGGACTGAGGTCACCTC 53146 | 286 286 | 3265 ACTGGCTGCAGGTCTTGGGCTTGCCCTTGAAGCCCTCTAGGTAGG | 286 286 | TCGGGCCAGGCACTCGCTGAGTGACCCCCAACATGCGGGTGAGCAGCTTAACCCCCTCTAGG 5 | aArqAlaArqHisSerLeuSerAspProAsnMetArq | 255 -MetAlaValLeuGluIleGlnThrAsnGlyAspThrAglThrGluGluAlaIleAl 274 | 3445 TCATAGCCTCTGCTTTGGCTCTACTCCATCTCACCATTTCCAATTTGTGCCCTGCACCCA 53386 | 254 254 | |
|---|------------|---|--|---|---|--|--------------------------|--|------------|---|--|--|--|----------------------------------|-----|--|--|---|--|--|--|--|---|---|--|------------------------------|--|--|---|---|--|---|
| Db 51406 ACCTCAGGGATGGTGCAGTAAGATGTGTTTTCCGGACTTCCCTTGGAGATGTCTACCATT 51347 | Qy 427 427 | Db 51466 CATTGTATTCATCATTCAGTACCCAACAGAAGGCTACTACTCTTGGAAGCCTTCCCTAAT 51407 | Qy 427427 | Db 51526 GTCTCTGCCTCTCTGTGTGTGTCTCTGTCTCTCTGTCCCTCTCTCCCTCTGG 51467 | Qy 427 427 | Db 51586 TGCTTTCCACAGTTCTCTTTCTCTGTCTCTGTCTCGCTGTCTGT | Qy 427 427 | Db 51646 CCTGCTCCTGGTGGCACCCCATTTTTCTGTACTGTTGCACCCCTGAGACACAGCATTTCCT 51587 | Qy 427 427 | Db 51706 AAAAAAAAAAAAAGAAAAGAAAAAGAAAAAGAAAAAGAAAA | Qy 427 427 | 51 | Qy 427 427 | 51 | 427 | 51886 TCAGCACACTAAATTCAAATGCCAGTCGTCTACATGTCCTGGATCCCAGCTGCACAGA | 427 | Db 51946 TICCCCATCTGGATCCAGAGCCATCACTCTGATCTCCCCCATCCTAGCTTCCATCCTTCC 51887 | Qy 427 427 | 52006 TITTACAGTCCTTCCCCATCCCATTGCGTGGTCTCTTCCATAGGCTTTTGGCCACCTCCA | | 52066 CTCCCCCAGGCTTCCAGAGACCAAATCCAAGCTGACCATTTTTTCCCCCAGAGGCTTCTTGC | 427 | AGAGTTAACCACAACCAGGAATGGGTGCCTCTGGGGACCTGTCTCTGTCCATCCCAATT | Ov 427 | 420 ProPheAspSerGluThrArgLyg | 52246 CCTCGTGTGTGCCCCACCCCCAGAGGGGCCCAAAAGGCCAAAACTCCAACCCCAGAA | Qy 400 ProArgValleuAlaProProGluGluValGlnLysAlaLysThrProThrProGlu 419 | 52306 ATCTCCAGGAATGGCATCTATCCACTCATGAATTTCGCTGCTCGGCCCTTGGGACTT | 382ArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgProLeuGlyLeu | TO TO TOTATO A TOTATO | 52426 TACTCAGAGGTTTCCTTCGTTGGAGCTGACAATTCCTAGAGGATGTCAGGTGAGAGCTG |

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VERSION
KEYWORDS
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AC115184
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Muzny, D. Marite, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Aydeji, M., Baca, E., Baden, H., Anyalebechi, V., Aoyagi, A., Aydeji, M., Baca, E., Baden, H., Anyalebechi, V., Aoyagi, A., Aydeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Brantead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Carzos, I., Ceasar, H., Center, A., Chen, Z., Chen, Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50986 CAGCCGACAGTGCCCAGGACCTCGCCGCCGAACTAGTGCACTATGGCTTCCTGCACGAGG 50927
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
1 (bases 1 to 248568)
MATTERIA. MATTERIA. Lee., Abramzon, S., Adams, C., Alder, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTTCCCCACCCCCTCCACTGCAGGATGACCGGACAAAGCTAGCAGCCTTTCTGGAGACC 5080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGGTTACATCGGCAGCTGACCTATGATCTGCTCCCAAGTAGGCTGGTAGGGGATCAGGT 51047
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Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Liz, Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lwis, L., Liz., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Martin, R., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Nurjhy, M., Nair, L., Nankervis, C., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Ffankoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Richards, S., Riggs, F., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shety, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Thomas, S., Tingey, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Tabor, P., Taylor, C., Valas, R., Warren, R., Waldron, L., Walker, B., Wang, J., Wang, J., Wang, J., Zhou, J., Zhou, Y., Zhang, J., Zhou, J., Zhou, Y., Zhang, J., Yoon, V., Willasana, D., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Willson, S., Tingey, A., Thomas, S., Tingey, A., Thomas, S., Tingey, A., Topor, J., Yoon, V., Warren, R., Walker, B., Wang, J., Yoon, V., Walker, B., Wang, J., Zhou, J., Zhou, Y., Zhang, S., Don, J., Yoon, V., Walker, B., Wang, J., Zhou, J., Zhou, S., Shith, J., Non, J., Yoon, V., Williams, G., Wilson, 
of Molecular and Human Geneme Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 6, 2002 this sequence version replaced gi:23267220. The sequence in this assembly is a combination of BRC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 248568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 248568) Worley, K.C.
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-- Genome Center

Web site: http://www.hgsc.bcm.tmc.edu/ Center: Baylor Co College of Medicine

Contact: hgsc-help@bcm.tmc.edu

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Percent Similarity:
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                                                                                                          GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg 40
                                                                                        GAGAGCGAGGACGACATCCTGGAGGAGAGCCCGTGTGGCCGCTGGCAGAAGCGG
                                                                                                                                                     ATGGCGGCCCCGGAGCCCGAGGAGAGGC-----CGGGAACGCGAGCGGGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                         ArgGluGlnVal----
                           CGGGAGCAGGT-GGGCACGGGTGCGGGTAACGCCACCGTCCCGTAGCCTAAGCATGGAGG 85795
                                                                                                                                                                       MetAlaAlaProGluProAlaProArgArgAlaArgGluArgGluArgGluArgGluArgGluAsp 20
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                                                                                                                                                                                                                                                 ACCATGTTTGAGCAGCTGGCGCTGGTGGACCACCCCAACATCGTCAAGCTGCACAAGTAT
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                                         GGAGTCGTGCGTCCGCTGCCAGGCCTGGAAGCGCTGGTGCACAGATCCTGTCTGCACT 86873
                                                                                                      TCAGGAGTGGGGTAGCGGGCGGCCTCCGCAGGCTCAGCCTCTTGGTGCCCACCCGAC 86813
                                                                                                                                                                GAGGGAGTCCAGCAGAACTTAGGGACAGTAGTGGGGCGGGGGACTCCGAGAGGCCTCGGT
                                                                                                                                                                                                                                                                                           CCGCAGGTCATCTTCATCACAGAATACGTGTCGTCTGGCAGCCTCAAGCAGTTCCTCAAA 8663
                                                                                                                                                                                                                                                                                                         AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLy8GlnPheLeuLy8 136
                                                                                                                                                                                                                                                                                                                                                      TGGCTGGATGCCTCTGAGGC-CCGCGAGGGTGAGCTAGGGGCGGGTGAAGGGCCGGAGT 86513
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                                                                                                                                                                                                                              AAGACCAAGAAGAACCACAAGGCCATGAACGCCCGGGTATGGGGAGTGGGTTGGGGACTG
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                                                                        -AlaTrpLysArgTrpCysThrGlnIleLeuSerAla-- 160
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                                                     GCTTCCCCACCCCCTCCACTGCAGGATGACCGGACAAAGCTAGCAGCCTTTCTGGAGACC 9017
                                                                                                                                                                                                                                                                                     CAGCCGACAGTGCCCAGGACCTCGCCGCCGACCTATGGCTCCTGCACGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTTCCCCTGCCACAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGC
ThrPheLeuLysTyrArgGlyThrGlnAla 507
                                                                                                                                                                     TGGGCGGGTGCGCCTCGGGTTTGGAAAGGTGCAGTCTGCCGAGCTGCCCAGTACTACCGT
                                                                                                                                                                                                                                                                                                                           -Thr-AspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGlu- 485
                                                                                                                                                                                                                                                                                                                                                                                                     GGTGGGCTGGGGCTCAGGCACCGGCTAGTGCCACAACTCACTTGTCCTGTGTTCTCTCTT
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                                                                                              -AspAspArgMetLysLeuAlaAlaPheLeuGluSer
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PUBMED
REFERENCE
AUTHORS
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COMMENT
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VERSION
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RS Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E. J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Fahey, J., Helton, E., Ketteman, M., Wadan, A., Rodrigues, S.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

D. 10,727,022 (1.00)
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Direct Submission
Submitted (23-yUN-2004) National Institutes of Health, Xe
Collection (XGC), National Institute of Child Health and
Development, 6100 Executive Boulevard, Room 4B01, Rockvil
                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 130 Row: o Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: DOE Joint Genome Institute, Walnut Creek,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project
Contact: XGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC074684 3046 bp mRNA linear Xenopus tropicalis nuclear receptor binding protein, clone MGC:69507 IMAGE:5336424), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus tropicalis (Silurana tropicalis)
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                                                                                                                                       /organism="Yenopus tropicalis"
/mal_type="mRNA"
/db_xref="taxon:8364"
/clone="MGC:69507 IMAGE:5336424"
                             clone_lib="NICHD_XGC_Emb7"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www.jgi.doe.gov
note="Vector: pCMV-SPORT6.1"
                                                                                                          tissue_type="Embryo, Silurana
                                                                                                             tropicalis,
                                                                                                                tailbud (stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRT 20-OCT-2004
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg
                                                                                      LeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThrSerAspThr
                                                                                                                                                  AsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGlnIleLeuSerAla
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                               IlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHisArgIlePheSer
                                                                                                                                                                                        TTCATCACAGAGTACATGTCCTCGGGGAGTCTCAAGCAGTTCCTCAAGAAGACAAAGAAA
                                                                                                                                                                                                     PheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLysLys
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                                                                                                                                                                                                                                                                                                         AAAATGCAGGAGGAGAAAGTGAAAGCCGTGTTTGATAATCTTATCCAGCTGGAGCATCTT
                                                                                                                                                                                                                                                                                                                      AlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuValAspHisPro
                                                                                                                                 AACCATAAAACCATGAATGAAAAGGCCTGGAAGAGGTGCTGCACGCAGATCCTCTCCGCT
                                                                                                                                                                                                                                                  AACATTGTCAAGTTCCACAAGTACTGGGCCGATGTGAAGGAGAACCGAGCCCGGGTCATC
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/protein_id="nuclear receptor binding protein"
/protein_id="nuclear receptor binding protein"
/db_xref="gi-49250536"
/db_xref="GeneID:448149"
/translation="MSEGEKTAPSTGSDPKMESGVSMSPPVSAPPAPPQEEEEEEEE
DESEILEESPOGRWOKRREEVNORNVPGIDSAYLAMDTEEGVEVVWNEVQFSERKNFK
MQEEKVKAVFDNLIQLEHLNIVKFHKYMADVKERRARVIFITEYMSSGSLKQFLKKTK
KNHKTWNEKAWKRWCTQILSALSYLHSCDPPIHGNLTCOIT FIQHNGLIKIGSVAPD
TINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDISFGMCALEMAVLEIGGNGESSY
VPQEAINNAIQFLEDPLOREFIQKCLETDPSKRFTARELLFHPALFEVFSLKLLAAHC
IVGHQHMIPENALEEMTKNLDMSAVLAEISHADREGVRNIFSQSPALELDKFLEDVRN
GIYPLTAFGVPRPQQPQQEVVKSPVPPSVKTATEPPEABVETTKVVQMQCNIESVDEG
AKHHLTLLKLEDKLNRHLSCDLLPNENIQELAAELVQLGFVSESDQIRLACLLEEAF
SKFYFARNGSMAAVTVSS"
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|codon_start=1
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BC004756 2128 bp mRNA line Mus musculus nuclear receptor binding protein, MGC:6961 IMAGE:3154089), complete cds. BC004756 BC004756.1 GI:13435803 MGC. MGC musculus (house mouse)
                                                                                                                                                                                                                                                          AlaAlaPheLeuGluSerThrPheLeuLysTyr 502
                                                                                                                                                                                                                      AspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAspArgMetLysLeu
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                                                                                                                                                                                                                                                                                                                   GlnCysAsnLeuGluArgSerGluAspLysAlaArgTrpHisLeuThrLeuLeuLeuVal
                                                                                                                                             GCCTGTTTACTTGAAGAAGCTTTCAGCAAGTTC
                                                                                                                                                                                                    GAGCTGGCAGCAGAGCTGGTACAGTTGGGCTTTGTCAGTGAGTCCGACCAGATTCGACTC
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                                                                                 linear
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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Strausberg,R.

Direct Submission

Submitted (21-MAR-2001) National Institutes of Health, Mammalian Submitted (21-MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, MD 20892-2590, Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: a Column: 1
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone was selected for full length sequencing because it
ad the following selection criteria: matched mRNA gi: 22219433
Location/Qualifiers
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                                                                                                                 217 IleArgAlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGlu
   237 ValAlaAsp---GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet 255
                                                                      762 GTGAAGACTTGCCGGGAAGAACAGAAGAACCTACACTTTTTTGCACCAGAGTATGGAGAA 821
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| Db 73 | Qy 19 | Db 68 | Οу 177 | Db 62 | Оу 157 | Db 56 | Qy 137 | pb 50 | Оу 117 | Db 444 | 2 40 | Db 384 | γQ | Db 324 | 9 | Db 264 | 0у з | Db 204 | 97 | US-10-618-941-99 | Alignment Sc pred. No.: Score: Percent Simi Best Local S Query Match: DB: |
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1344 GTTGTGCCCCCCCTCTGTCAAGACTCCAACTCCTGAGCCAGCTGAAGTGGAGACACGAAAG 1403
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                                                                                    1524 GAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGAT 1583
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                                                                                                                                468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      942 AGTGCCATCCAGCTACTAGAAGACTCATTACAGAGGGAGTTTATTCAAAAGTGCCTGCAG 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 ArgAlaArgHisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        882 GCAGTGCTGGAGATTCAGGGCAATGGCGAGGAGTCCTCATATGTGCCACAGGAAGCCCATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 AlaValLeuGluIleGlnThrAsnGlyAspThrArg---ValThrGluGluAlaIleAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuAspLysPheLeuGluAspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAla 393
                                                                                                            AspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAsp 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProArg---ProArgArgProProLeuGlnTrpArgTyrSerGluValSerPheMetGlu 373
                                                                                                                                                                                                                                                                                                                                                                           ------GlnLysAlaLysThrProThrProGluProPheAspSerGluThrArgLys 427
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Search completed: January 13, 2006, 23:36:28 Job time: 6726 secs

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US-08-933-750C-69

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US-09-234-613-69

US-09-023-1428

US-09-023-1428-15-1939

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US-09-949-016-13170
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Sequence 1053, Ap
Sequence 9, Appli
Sequence 9, Appli
Sequence 69, Appl
Sequence 69, Appl
Sequence 1428, Ap
Sequence 9, Appl
Sequence 1939, Ap
Sequence 13370, A
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| 5916 | 5820 | 5820 | 5736 | 5736 | 2949 | 2949 | 2865 | 2865 | 2769 | 2769 | 2685 | 2685 | 2490 | 2490 | 2406 | 2406 | 2310 | 2310 | 2226 | 2226 | 334 | 334 | . 260 | 669 | 669 | 669 | 669 | 669 | 669 | 669 | 669 | 669 | 669 | 669 | 669 |
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| o w | equence 47, | equence 47, | equence 63, | equence 63, | equence 5, | equence 5, | quence 21, | e 21, | quence 37, | e 37, | e 53, | equence 53 | equence 11, | equence 11, | equence | equence | equenc | equence 43 | equence | equence 59, | equence 153 | equence 104 | equence 978 | equence 23, | equence 23, | equence 23, | equence 23, | equence 23, | equence 23, | equence 23, | equence 23, | equence 23, | equence 23, | equence 23, | • |
| App1 | Appl | App1 | App1 | Appl | Appli | Appli | Appl | Appl | Appl | Appl | Appl | Appl | App1 | Appl | App1 | Appl | Appl | App1 | Appl | Appl | 86, A | App | , App | App1 | App1 | App1 | App1 | Appl | App1 | App1 | Appl | Appl | Appl | Appl | Appl |

ALIGNMENTS

RESULT 1 US-09-976-594-1053

Sequence 1053, Application US/09976594 Patent No. 6673549

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US-10-618-941-99 (1-507) x US-09-976-594-1053 (1-4048)
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Best Local Similarity:
Query Match:
                                                                                                                                                        Pred. No.:
                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
APPLICANTON: GENER EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT FILING DATE: 2001-10-12
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 1053
LENGTH: 4048
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               LysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeuProArgProArgArgPro
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 AAGA CCAAGG CCATGGA CCTGCA CGCGGT CTTGG CGGAGCTT CCCCGGCCCCGCAGGCCC
                                                                                                                     CCCTCTGCCCACAGCCTCCTCCTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAAGCTC
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; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (981)
; OTHER INFORMATION: n = A
US-09-345-473E-9
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Patent No. 6558903
GENERAL INFORMATION: NO. 6558903el Kinases and TITLE OF INVENTION: NO. 6558903el Kinases and FILE REFERENCE: 35800/183781
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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                             GAGAGCGAGGACGAGCGACATCCTGGAGGAAAGCCCCGTGTGGTCGCTGGCAAAAGCGA
                                                                                      ATGGCGGCCCCGGAGCCGCGAGGCGGGAGCCGGGAACGGGAGCGGGAGCGGAACGAC
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APPLICANT: HOGGE, MARTIN R.
TITLE OF INVENTION: NO. 6858418el Kinases and FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR TILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                    Sequence 9, Application US/09862027
Patent No. 6858418
GENERAL INFORMATION:
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; LENGTH; 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1).T.(981)
; OTHER INFORMATION: n=A,T
US-09-862-027-9
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| Alignment Scores: Pred. No.: 1.13e-159 Score: 1534.50 Percent Similarity: 73.54% Conservative: 59 Percent Similarity: 61.62% Mismatches: 102 | ; STRANDENESS: single ; TOPOLOGY: linear ; IMMEDIATE SOURCE: ; LIERARY: BRAITUT03 ; CLONE: 864683 US-08-933-750C-69 | INFORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS: LENGTH: 2029 base pairs TYPE: nucleic acid | | ATTORNEY/AGENT INFORMATION: , NAME: Billings, Lucy J., REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0356 US | ON: 536 ION DATA NUMBER: | SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/933,750C FILING DATE: September 23 1997 | 5398 | φ <u>.</u> | ticals, Inc. | APPLICANT: Yue, Henry APPLICANT: Guegler, Karl J. APPLICANT: Corley, Neil C. TITLE OF INVENTION: HUMAN REGULATORY MOLECULES | APPLICANT: Hillman, Jennifer L. APPLICANT: Bandman, Olga APPLICANT: Shah, Purvi APPLICANT: Shah, Purvi APPLICANT: AL-Young. Janice | Ce 69, A No. 593 AL INFOR | Db 977 CCTG 980 RESULT 4 US-08-933-750C-69 | 320 uLeu 321 | Qy 301 ProSerAlaHisSerLeuLeuPheHis-ArgValLeuPheGluValHisSerLeuLysLe 320 | Qy 281 SerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspProAlaArgArg 300 | Db 797 CAGACCAATGGGGACACCCGGGTCACAGAGGAGGCCATTGCTCGCCGGCCAGGCACTCGCTG 856 |
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| 335 GluasnValValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeu | Qy 295 ArgAspProAlaArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGlu 314 | Qy 275 ArgAlaArgHisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAla 294 | Qy 256 AlaValLeuGluIleGlnThrAsnGlyAspThrArgValThrGluGluAlaIleAla 274 | Qy 237 ValalaaspGlyThralaValaspIlePheSerPheGlyMetCysAlaLeuGluMet 255 | Qy 217 IleargalaGluargGluGluLeuargAsnLeuHisPhePheProProGluTyrGlyGlu 236 | Qy 197 ArgIlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro 216 | Qy 177 ThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHis 196 | Qy 157 IleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeu 176 | Qy 137 LysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln 156 | Oy 117 AlaArgValllePhelleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys 136 | Qy 97 ValaspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCys 116 | Qy 77 ArgLysAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeu 96 | Qy 57 LeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAsp 76 | TGCCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATAC | 240 | US-10-618-941-99 (1-507) x US-08-933-750C-69 (1-2029) Qy 17 GluargGluaspGluserGluaspGluserAspIleLeuGluGluSerProCysGlyarg 36 | Query Match: 57.47% Indels: 29 DB: 2 Gaps: 6 |

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Sequence 69, Application US/09234613

Patent No. 6132973

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.

APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.

APPLICANT: Guegler, Karl J.

APPLICANT: Gorley, Neil C.

TITLE OF INVENTION: HUMAN REGULATORY MOLECULES

NUMBER OF SEQUENCES: 98

CORRESPONDENCE APPLICA
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US-09-234-613-69
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOPTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                          STREET: 3174 POIL
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
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SEQUENCE CHARACTERISTICS:
LENGTH: 2029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT03
CLOME: 864683
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                       AlaValLeuGluIleGlnThrAsnGlyAspThrArg---ValThrGluGluAlaIleAla
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                                                                                          ValAlaAsp---GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet
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   GCAGTGCTGGAGATTCAGGGCAATGGAGAGTCCTCATATGTGCCACAGGAAGCCATCAGC
                                                                       GTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGGCATGTGTGCACTGGAGATG
                                                                                                                                              GTGAAGACTTGTCGAGAAGAGCAGAAGAATCTACACTTCTTTGCACCAGAGTATGGAGAA
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FABSUSED for Windows Version 4.0

SEQ ID NO 1428

LENGTH: 2163
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US-09-949-016-1428
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TYPE: DNA
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                                                                                                          ArgAlaArgHisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAla 294
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                                                                                                                                                                     GCAGTGCTGGAGATTCAGGGCAATGGAGAGTCCTCATATGTGCCACAGGAAGCCATCAGC
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Matches:
Conservative:
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RESULT 7
US-09-023-942A-9
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GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Ton
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILLING DATE: 13-FEB-1998
CLASSIFICATION: 435
PILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Internation:
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: (US only) ANTALIS TONI Marie and I
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PO5101/97
                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 11530
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                                                         International
                                                                                                                                                                                                                                                                                          Version
                                                         PCT Application
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-618-941-99 (1-507) x US-09-023-942A-9 (1-2241)
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENCTH: 2241 base pairs
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TOPOLOGY: linear
MOLECULE TYPE: DNA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEPAX: (516) 742 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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LOCATION:
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                                   GTGAAGACTTGTCGAGAAGAGCAGAAGAATCTACACTTCTTTGCACCAGAGTATGGAGAA
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ValAlaAsp----GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet
                                                             IleArgAlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGlu
                                                                                                                                                   ArgIlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro
                                                                                                                                                                                                                  ThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHis 196
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Matches:
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241el full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2002-03-25
PRIOR FILING DATE: SPATENTE OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1939
LENGTH: 2546
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                             RESULT 8
US-10-104-047-1939
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                                                                                                                                                                                               Sequence 1939, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
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RESULT 9
US-09-949-016-13170
; Sequence 13170, Ap;
; Patent No. 6812339
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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| OY 111 111 Db 7485 ATTGCAAAGAGACTAGCTACATTTATTATTGTTCCTTTTACACTCAGAGATTAAAACAAG 7544 OY 111 111 Db 7545 GTAGTTTTGAAACAGAACTGGAATCAGCTGCAATGGCGATAAGAGTAGGGCTTCAGTTGT 7604 | | Qy 84 | Db 7185 GGGGAATGTTGGAACACTGATGTTAGAGAGGAATTGGTGTTGGGAAGCTGCCCGTGAGGA 7244 Qy 83 | Qy 74 PheGlyAspArgLysAlaPhe-AlaAlaHis | Oy 54 SerThrPheLeuAlaMetAspThrGluGlyUalUalUalUalTrpAsnGluLeuHis 73 ::: | Db 6945 TGGGGGCTAGGAGGAGTGATCATATGGAGTGTTAAAATGGAGGATTTGTGAGATAAGTT 7004 Oy 43GlnValabbuglugluglugluglugluglugluglugluglugluglu | QY 42 | DD 6765 GAGGAAGAAGAAGATGAAGATGAGTCTGAGATTTTGGAAGAGTCGCCCTGTGGGCGC 6824 Qy 37 TrpGlnLysArgArgGlu | -10-618-941-99 (1-507) x US-09-949-016-13170 (1-17616) 17 GluhrgGluhspGluserGluhspGluSerhapIleLeuGluGluSerProCyaGlyArg | Allgnment Scores: 7.3e-34 Length: 17616 Pred. No.: 7.3e-34 Length: 17616 Score: 413.50 Matches: 134 Percent Similarity: 25.41% Conservative: 21 Best Local Similarity: 21.97% Mismatches: 22 Query Match: 15.49% Indels: 435 DB: Gaps: 6 | ; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 13170 ; LENGTH: 17616 ; TYPE: DNA ; ORGANISM: Human US-09-949-016-13170 |
|--|--|--|--|--|--|--|---|--|---|--|--|
| Oy 185 isAsmGlyLeuIleLySer 193 | 8443 CCCCTGCCCTTAATTTCCCAGTGGCC 165 isAlaCysSerProProIleIleHist | GATTATCTTTATGGTGACCAGCAGGAGACCTGGCCCTTGCTCCTCTTAACCCTTGGGTTC | 161 | TGTTCTATTCTGCCTCTCCCCACTTTCTTTGAATCATATACTGTCAAGATTAGGGCCCCT | Qy 161 161 Db 8143 GTTTCTTACCCATATTTCCTGATGTTACTCCAAACAGATTTCAGGGCACTACTCTTC 8202 | Db 8023 CTAGTGGGAGAGTTAAGAGAGGGAATTACTGCTGACCCTTGGATCCAACTTTGTTCCA 8082 Oy 149 -AlaTrpLysArgTrpCysThrGlnIleLeuSerAlaLeu | 7963 GGGGTGGTTTTAAAAAGGACTCTGTTAATAATGAAGCTGATCAGGAAGGGACGGAAGGAG | Oy 142 sLysAlaMetAsnAlaArg 148 | 122 eThrGluTyrValSerSerGlySerLeuLygGlnPheLeuLygLygThrLygLygAgnHi | Qy 116 116 Db 7724 AAGAACAAAAGGAGAAAATTTTAACAAACCTTCAAATTTAAAAATATGTTAACAAGGGAA 7783 Qy 117 | Qy 111 111 Db 7605 CACCTATGCCTTTTGTGTGGCTATAGATTGGGCAGAAATGAGTGAACTTTTGCTTCTTT 7664 Qy 112 116 |

GENERAL INFORMATION:

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Best Local Similarity:
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SOFTWARE: FASESEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,984
FILING DATE: 18-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
TYPE: nucleic acid
STRANDEDESS: single
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APPLICANT: Wang, TongTong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF LUNG CANCER
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                   GTCAAACACCACCTGACACTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGC
TyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGly 481
                                                    AlaArgTrpHisLeuThrLeuLeuLeuValLeuGluAspArgLeuHisArgGlnLeuThr
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US-09-123-912-23
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Patent No. 6312695
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NAME/KEY: modified_base
LOCATION: (642)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
LOCATION: (661)
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APPLICANT: Wang, Tongtong
ITTLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
PRIOR APPLICATION NUMBER: 09/040,802
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
COMPTANDE OF SEQ ID NOS: 114
COMPTANDE OF SEQ ID NOS: 114
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TYPE: DNA
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APPLICANT: Skeiky, Yabil 7.....

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: MCNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C11

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 369

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 23

LENGTH: 669
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Patent No.
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NAME/KEY: misc_feature
LOCATION: (1)...(669)
OTHER INFORMATION: n =
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TYPE: DNA
ORGANISM: Homo sapien
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                                                GTCAAACACCACCTGACACTT
                                                               AlaArgTrpHisLeuThrLeuLeuLeuValLeuGluAspArgLeuHisArgGlnLeuThr 461
                                                                                                          GAGGTGGAGACTCGCAAGGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGA
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Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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Skeiky, Yasir A.W.
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Bangur, Chaitanya S.
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APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Fan, Liqun

APPLICANT: Kalos, Michael D.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C6

CURRENT APPLICATION NUMBER: US/09/480,884A

CURRENT FILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 330
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LOCATION: (1)...(669)
OTHER INFORMATION: n =
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ORGANISM: Homo
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APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FO
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
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SEQ ID NO 23
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TYPE: DNA
ORCANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(669)
OTHER INFORMATION: n = 1
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Fan, Liqun
Kalos, Michael D.
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LOCATION: (1)...(669)
OTHER INFORMATION: n =
US-09-606-421B-23
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Best Local Similarity:
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitar
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R
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CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 669
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GENERAL INFORMATION:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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ORGANISM: Homo sapien
FEATURE:
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                                                                                                  TGTGACCTGATGCCAAATGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGC
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Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
                                 TTCATTAGTGAGGCTGACCAGAGCCGGTTGACTTCTCTGCTAGAAGAGAGCT
                                                               PheLeuHisGluAspAspArgMetLysLeuAlaAlaPheLeuGluSerThr 498
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Bangur, Chaita
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Search completed: January 14, 2006, 00:50:21 Job time: 275 secs

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GERERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAENEPEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT FILING DATE: 2003-07-15
PRIOR REPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
VUMBER OF SEQ ID NOS: 143
SOFTWARE: PRECENTIN VERSION 3.2
SEQ ID NO 99
LENGTH: 507
TYPE: PRT
ORGANISM: Homo sapiens
Reverse Translation from the peptide US-10-618-941-99.
NOTE: the original peptide US-10-618-941-99 contained at least one of thus contains ambiguous bases which may translate into amino acids thus cother than the original amino acids.
US-10-618-941-99
ATGCCNOCOMBARCANGNCONGNGNGNGNGNARMGNGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGANGNARGAN
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GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
CURRENT FILING DATE: 2003-07-15
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOFTMARE: PAtentin version 3.2
SOFTMARE: PAtentin version 3.2
SEQ ID NO 99
LENGTH: 507
TYPE: PRT
ORGANISM: Homo sapiens
US-10-618-941-99
WAAPEPAPRAREREREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGV
EVWNELLFGDIKAFAAHEEKIQTVFEGLVLVDHFNIVKLHKYMLDTSERCARVIFITEVSSGS
LKQPLKKTKNHKAMNARAMKRWCTQILSALSFILAGSPFIIHGNLTSDTIFIQHNGLIKIGSVW
HRIFSNALRPTALPDDLRSPIRARESLRNLHFFPPEVGLVEVHSLKLIAAHC
FIOHQYLMPENVVEEKTKAMDLHAVLAELPRPRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMN
FAATRPJGLRRALAGASDLASELVHYGFLHEDDRMKLAAFLESTFLKYRGTQA1
LHRQLTYDLLPTDSAQDLASELVHYGFLHEDDRMKLAAFLESTFLKYRGTQA1
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           Pred. No. is the number of results predicted by chance to n score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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| UB=Corpora Med=11218 ., Shibbata Fukunishi Nishi K., Gojobori A., Ashbur eriand T., F, Suzuk uruno M., , Bojung C., Fletc C., Fletc C., Hofmann L., Mashim Ringwald M., hida K., H hida K., | RRY; 1. 23, 1. 2 | 0000HH0000000 |
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A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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B Submitted (JUL-201) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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Sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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MGI; MG
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ProDom; PD00001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Nucleotide-binding; Receptor; Transferase SEQUENCE 547 AA; 61221 MW; 57462EA3936E2762 CRC64;
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GO:0005524; F:ATP binding; IEA.
GO:0004672; F:protein kinase activity; IEA.
GO:0004872; F:receptor activity; IEA.
GO:0004872; F:rransferase activity; IEA.
GO:0016740; F:rransferase activity; IEA.
GO:0006488; P:protein amino acid phosphorylation;
GO:0006488; P:protein amino acid phosphorylation;
erPro; IPR0000719; Prot_kinase.
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human rand movine colons and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGGL31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                       FISSUE=Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc.
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XENTR
mitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

IL; BCO74684; AAH74684.1; RNA.

GO:0005524; F:ATP binding; IEA.

GO:0004674; F:protein serine/threonine kinase activity;

GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO:0004872; F:receptor activity; IEA.

GO:00064872; F:receptor activity; IEA.

GO:0006469; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVIMQCNIESVEEGVKHHLTLLKLEDKLNRHLSCDLMPNESIPDLAAELGQLGFISEAD
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                                                                                                                                                                                                                                                                                                                                  Gerhard D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Best Local S
Matches 306
NUCLEOTIDE SEQUENCE.
STRAIN129, and FVB/N;
TISSUE=Mammary tumor. Brcal-/fl, and Mammary tumor. C3;
TISSUE=Mammary tumor. Brcal-/fl, and Mammary tumor. C3;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Creat
01-JUN-2001 (TrEMBLrel. 17, Last
10-MAY-2005 (TrEMBLrel. 30, Last
Nuclear receptor binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000001; Prot
SMART; SM00220; S_TKC;
SMART; SM00219; TyrKc;
                                                                                                                      Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Eu
Muridae; Murinae; Mus
                                                                                                                                                                                                                                                     Q99J45_MOUSE
Q99J45;
                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                          Name=Nrbp;
                                                                                                                                                                                        kinase)
                                                                                                                                                                                                                                                                              MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                              --KTPTPEPFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPPEEVQKA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FITEYMSSGSLKQFLKKTKKNHKTMNEKAMKRWCTQILSALSYLHSCDPPIIHGNLTCDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSAP-PAP----PQEEEEEESEDESEILEESPCGRWQKRREEVNQRNVPGIDSAYLAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAAPEPAPRRAREREREREDESEDESDILEESSPCGRWQKRREQVNQGNMPGLQSTFLAMD
                                                                                                                                                                                                                                                                                                                                                                                 SVKTPTPEPAEVETRKVVQMQCNIESVDEGAKHHLTLLLKLEDKLNRHLSCDLLPNENIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                     REGVRMI FSQSPALELDKFLEDVRNGI YPLTAFGVPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRPTARELLFHPALFEVPSLKLLAAHCIVGHQHMIPENALEEMTKNLDMSAVLAEISHAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFIQHNGLIKIGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEEGVEVVWNEVQFSERKNFKMQEEKVKAVFDNLIQLEHLNIVKFHKYWADVKENRARVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001245; Tyr pkinase
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                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59285
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59.9%;
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                                                                                                                                                                                                 sequence update)
annotation update)
(HLS7-interacting
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An Distchenko L., Marusina K., Farmer A.A., Rubin-G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
An Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
An Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
An Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
An Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
An Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
An Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
An Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
An Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
An Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
An Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
An Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
An Hiting M., Madan J.W., Green E.D., Dickson M.C.,
An Hiting M., Krzywinski M.I., Schutz J., Myers R.M.,
An Hotterfield Y.S.N., Krzywinski M.I., Schutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 307
                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.

C STRAIN=BDF1;

C STRAIN=BDF1;

A McCulloch R., Lim R., Ingley E., Williams J., Klinken S.P.

A McCulloch R., Lim R., Ingley E., Williams J., Klinken S.P.

A McCulloch R., Lim R., Ingley E., Williams J., Klinken S.P.

A McCulloch R., Lim R., Ingley E., Williams J., Klinken S.P.

A McCulloch R., Lim R., Ingley E., Williams J., Klinken S.P.

B Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC018463; AAH018463.1; -; mRNA.

EMBL; BC018463; AAM97260.1; -; mRNA.

R EMBL; AF302139; AAK97261.1; -; Genomic DNA.

Ensembl; ENSMUSGO000029148; Mus musculus.

R MGI, MGI: A18346; ALPD.

R GO: GO:0005524; F:ATP binding; IEA.

R GO: GO:0004872; F:protein kinase activity; IEA.

R GO: GO:0004872; F:receptor activity; IEA.

R GO: GO:0004872; F:transferase activity; IEA.

R GO: GO:0004872; F:transferase activity; IEA.

R GO: GO:0004872; F:receptor activity; IEA.

R Frosories F. Solonies F. Transferase; I.

R ProDom; PD000001; Prot kinase; I.

R ProDom; PD000001; Prot kinase; I.

R ATP-binding; Kinase; Nucleotide-Finding; Receptor; Transferase; I.

S GO: GO:0005874; F:receptor GO:00
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STRAIN=BDF1, and 129;
MEDLINE=22287351; PubMed=12176995; DOI=10.1074/jbc.M206041200;
MEDLINE=22287351; PubMed=12176995; DOI=10.1074/jbc.M206041200;
Lim R., Winteringham L.N., Williams J.H., McCulloch R.K., Ingle
Tiao J.Y.-H., Lalonde J.P., Tsai S., Tilbrook P.A., Sun Y., Wu
MOTRIS S.W., Klinken S.P.;

"MADM, a novel adaptor protein that mediates phosphorylation of
14-3-3 binding site of myeloid leukemia factor 1.";
J. Biol. Chem. 277:40997-41008(2002).
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Director MGC F
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STRAIN=129; TISSUE=Mammary
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                                                                                                                                                                                                                                                                      Similarity
                                           RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQELK
                                                                                                                                              KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH
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                                                                                                                                                                                                                                               Score 1537.5; DB 2;
Pred. No. 1.7e-102;
B; Mismatches 105;
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RESULT 4

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AC Q8NC
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                                                                                                                                                                                                                                        Query Match
Best Local !
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Ensembl; ENGG00000185189; Homo sapiens.
HGNC; HGNC:19339; NRBP2.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:00064678; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot kinase.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last samotation updat
01-OCT-2003 (TrEMBLrel. 25, Last samotation updat
Hypothetical protein DKFZp434I2411 (Fragment).
Name=NRBP2; Synonyme=DKFZp434I2411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid
Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
NON TER 1
SEQUENCE 294 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
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ARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLM
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RX PubMed=14702039 DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Ota T., Suzuki Y., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Sairatori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E.,
RA Sugawara M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
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RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Wajiyi Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sagano S.,
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MEDLINE=20304761; PubMed=10843813; DOI=10.1006/geno.2000.6167;
MEDLINE=20304761; PubMed=10843813; DOI=10.1006/geno.2000.6167;
Hooper J.D., Baker E., Ogbourne S.M., Sutherland G.R., Antalis T.N.
"Cloning of the cDNA and localization of the gene encoding human national positionally expressed, multidomain putative adapter protein.";
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Multiple domain putative nuclear protein (Hypothetical protein
FLJ11084) (Hypothetical protein DKFZp564D1878) (Nuclear recepto
binding protein) (Hypothetical protein NRBP).
Name=BCON3; Synonyms=DKFZp564D1878, NRBP;
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01-MAY-2000 (TrEMBLrel. 13,
13-SEP-2005 (TrEMBLrel. 31,
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Mammalia; Eutheria;
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                        36:40-45(2004)
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Strausberg R.D., Collins F.S., Wagner L.H., Shemmen C.M., Schuler G.D.,
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RX Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RX Ahley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX Ahleny J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RX RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RX "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA semences."
Query Match 57.5%;
Best Local Similarity 61.6%;
Matches 305; Conservative
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Submitted
                                                                                     ProDom; PD000001; Prot kinase; 1.

PROSITE; P850011; PROTEIN_KINASE_DOM; 1.

ATP-binding; Hypothetical protein; Kinase; Nuclear protein; Nucleotide-binding; Receptor; Serine/threonine-protein kina
                                                                                                                                                              GO; GO:0005634; C:nucleus; TAS.
GO; GO:0005070; F:SH3/SH2 adaptor activity;
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IRR000719; Prot kinase.
Pfam; PF00069; Pkinase; 1
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Submitted (APR-2005)
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Submitted (SEP-2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
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id C., Osanger A., Fobo G., Han M
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Score 1534.5; DB 2
Pred. No. 2.7e-102;
9; Mismatches 102;
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Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                    International consortium for macaque "DNA sequences of macaque genes expre evolutionary implications.";
Submitted (JUN-2005) to the EMBL/GenR
                                                                        Receptor.
SEQUENCE
                                                                                                                   Osada N., Hirāta M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.; "Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs."; Submitted (WAR-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AB168327; BAE00451.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i3-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sunctation update)
13-SEP-2005 (TrEMBLrel. 31, Last sunctation update)
Testis cDNA clone: QtsA-11263, similar to human nuclear binding protein (NRBP), (Brain cDNA, clone: QnpA-17237, human nuclear receptor binding protein (NRBP),).
Macaca fascicularis (Crab eating macaque) (Cynomolgus mo
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Mammalia; Butheria; Buarchontoglires; Primates;
Cercopithecidae; Cercopithecinae; Macaca.
NCBI_TaxID=9541;
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Score 1534.5; DB 2
Pred. No. 2.7e-102;
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OF STANDARD TO STA
TA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., & Fobo G., Han M., Wiemann S.; LL Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases. EMBL; CR858669; CAH90881.1; -; mRNA. B. GO; GO:0004574; F:ATP binding; IEA. GO; GO:0004674; F:protein serine/threonine kinase activity; IEA. GO; GO:0004713; F:protein-tyrosine kinase activity; IEA. B. GO; GO:0004740; F:transferase activity; IEA. B. GO; GO:0004740; F:transferase activity; IEA. B. GO; GO:0006468; P:protein-amino acid phosphorylation; IEA. B. GO; GO:0016740; F:transferase. B. InterPro; IPR000719; Prot kinase. B. InterPro; IPR000719; Prot kinase. B. InterPro; IPR001245; Tyr_pkinase. B. InterPro; IPR001245; Tyr_pkinase. B. InterPro; IPR001245; Tyr_pkinase. B. FroDom; PD000001; Prot_kinase. B. FroDom; PD000001; Prot_kinase. B. FroDom; PD000001; Prot_kinase. B. R. FroDom; PD00001245; Tyr_pkinase. B. R. FroDom; PD00001245; Tyr_pkinase. B. R. SMART; SM00220; S_TKC; 1.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence up
01-FEB-2005 (TrEMBLrel. 29, Last annotation
Hypothetical protein DKFZp459G2032.
Name=DKFZp459G2032;
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The German cDNA Consortium;
Occupan A Mewes
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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NCBI_TaxID=9600;
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Best Local Similarity
Matches 305; Conser
                                                                                                                                                                                                                                                                                                                                                                     Homo.
NCBI_TaxID=9606;
                                                                                    Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y. Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawar Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguch Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                         Name=NNUBF;
HOMO SARIBORS (Human).
Eukaryota; Metazoa; Chordata; Craniata; Verteuzo
Eukaryota; Metazoa; Chordata; Craniata; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Hypothetical protein FLJ14632.
Name=NRBP;
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Q96SU3;
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SEQUENCE 535 AA; 59818 MW; 398078
                                        EMBL;
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                                        (xeno); NbExp=1;
8; BAB55185.1; -
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Pred. No. 2.7e
59; Mismatches
                                        IntAct=EBI-465766, mRNA.
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25 HUMAN
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Nuclear receptor binding protein var
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larity 61.4%;
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Pred. No. 6.3e-102;
9; Mismatches 103;
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Tanaka A., Yokoyama S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ
EMBL; AKZ23136; BAD96856.1; -; mRNA.
HGNC; HGNC:7993; NRBP.
GO; GO:0005524; F.ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine ki
GO; GO:0004713; F:protein-tyrosine kinase act
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0006468; P:protein amino acid phosphor
                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suzuki Y., Yoshitomo K., Maruyama I "Construction and characterization end-enriched cDNA library.";
Gene 200:149-156(1997).
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Suzuki Y., Yos
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Gene 138:171-174(1994).
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QSRLTSLLEETLNKF
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-; mRNA.
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I Genome Biol. 6.R6-R6(2005).

R EMBL; AJ721116; CAG32775.1; -; mRNA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004674; F:pxotein serine/threonine kinase activity; IEA.

R GO; GO:0004713; F:pxotein-tyxosine kinase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016740; F:transferase

GO; GO:0016740; F:transferase

R InterPro; IPR002719; Prot kinase.

InterPro; IPR002290; Ser_Ehr_pkinase.

R InterPro; IPR002291; Ser_Ehr_pkinase.

R InterPro; IPR001245; Tyx pkinase.

R InterPro; IPR000291; Tyx pkinase; 1.

R Pfam; PF00069; Pkinase; I.

R Pfam; PF00069; Pkinase; I.

R Pfam; PF000101; Protekinase; 1.

R SMART; SM00219; TyrKc; 1.

R SMART; SM00219; TyrKc; 1.

R Hypothetical pxotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel.
Hypothetical protein.
ORFNames=RCJMB04_35j18;
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SEQUENCE 5:
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SEADQSRLTCLLEEAFSKFYYTR
                                                                                                                    ETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFL
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                                          HEDDRMKLAAFLESTFLKYRGTQ 506
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                                                                                           ETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLQPNDNIQELAAELVQLGFI
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Pred. No. 3.6e-101;
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RX MEDILINE-2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F. Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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Query Match
Best Local Similarity
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Q6NTZ7;
05-JUL-2004 ('05-JUL-2004 ('
                                                                                                         Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; TKC; 1.
SMART; SM00219; TYTKC; 1.
PROSITE; PS50011; PROTEIN KINASE
SEQUENCE 526 AA; 59366 MW; E9
                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein S., Strausberg R.;

Submitted (Apr-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; BC068805; AAH68805.1; -; mRNA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity;

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; P:cell division; IEA.

GO; GO:000648; P:protein anino acid phosphorylation; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla, Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=MGC81395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genetic and genomic tools initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissue=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225:384-391 (2002).
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   56.7%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A. 99:16899-16903(2002)
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27,
27,
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       Score 1514;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus
                                                                                                     E966F6C5FCBC742B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         research: The NIH Xenopus
                                         DB 2;
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                                         526;
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TO SHOW THE PROPERTY OF THE PR
                                    Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases
EMBL; AL554831; CAIZO617.1; -; Genomic_DNA.
GO; GO:0005524; F:ATD binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activ
GO; GO:0004673; F:protein-tyrosine kinase activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004868; P:protein amino acid phosphorylation; 1
InterPro; IPR00279; Prot kinase.
InterPro; IPR00229; Ser Ehr_pkinase.
InterPro; IPR00229; Ser Ehr_pkinase.
PFD007; PP00069; Pkinase; 1.
SMART; SM00219; TyrKc; 1.
SMART; SM00219; TyrKc; 1.
SMART; SM00219; TyrKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; C
Actinopterygii; Neopterygii; Te
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                      (1)
NUCLEOTIDE
Phillimore
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01-FEB-2005
01-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q5SNQ3_BRARE
Q5SNQ3;
                            PROSITE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORFNames=DKEY-12H9.7-001;
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BRARE
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 29, Created)
(TrEMBLrel. 29, Last sequence update)
(TrEMBLrel. 29, Last annotation update)
in similar to vertebrate nuclear recep
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                          PROTEIN_KINASE_DOM;
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                                                                                                                                                                                                                                                                                                                                                                                                                ) (Danio rerio).
; Craniata; Vertebrata; Eu
Teleostei; Ostariophysi;
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                                                                                                                                                                                phosphorylation; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
i; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding
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NUCLEOTIDE SEQUENCE.

Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.

A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.

A Anthouard V., Jubin C., Castelli V., Katinka M., Vacherle B.,

A Anthouard V., Jubin C., Cattolico L., Poulain J., De Berardinis V.,

A Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

A Cruaud C., Duprat S., Brottler P., Coutanceau J.P., Gouzy J.,

A Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.

A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.

A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

A Kellis M., Schachter V., Quetier F., Saurin W., Scarpelli C.,

A Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (
13-SEP-2005 (
13-SEP-2005 (
Chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q4S1G5;
                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleoste
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment)
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ProDom; PD000001; Prot_kinase; 1.
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-i-CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
-i-FUNCTION: Plays a key role in the control of the eukáryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of the Subunit; Forms a stable but non-covalent complex with cyclin B in mature.
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EMBL; CAAE01014768; CAG05517.1; -; Ge
InterPro; IPR0007719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

Nuclear Submitted (JUN-2004) to the EMBL/GenBank/DDBJ datal

EMBL, AL137662; CAB70864.1; -; mRNA.

EMBL; CR457350; CAG33631.1; -; mRNA.

PIR; T46491; T46491.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004672; F:protein amino acid phosphorylatic

InterPro; IPR000719; Prot_kinase.

ProDom, PD000001; Prot_kinase.
(Fragment).

(Fragment).

ORFNames=GSTENG00032841001;

ORFNames=GSTENG00032841001;

Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                             Q4RKP5_TETNG
Q4RKP5;
13-SEP-2005 ('
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13-SEP-2005 ('
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Q9NSYO;
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01-OCT-2000 (
01-FEB-2005 (
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01-OCT-2000 (TrEMBLrel. 15, Last sequence upd
01-FEB-2005 (TrEMBLrel. 29, Last annotation u
Hypothetical protein DKFZp434P086 (LOC340371;
Name=DKFZp434P086; Synonyms=LOC340371;
Homo sepiens (Human)
                                                                                                                                                                                                                                                    Chromosome 5
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Submitted (JAN-2000)
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Mammalia; Eutheria;
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whole genome shotgun sequen
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EMBL/GenBank/DDBJ
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Pred. No. 4.4e-89;
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rimates; Catarrhini;
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databases.
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RP NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Diemont C., Salanoubat M., Levy M., Boudet N., Castellano S.,

RA Anthousard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Duprat S., Hortier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Duprat S., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Cruaud G., Larder G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander B.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

RT the early vertebrate proto-karyotype.";

RA Nature 431:946-957(2004).
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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1- FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of MPF (By similarity).

MPF (By similarity).

mature occytes (By similarity).

EMBL; CAAB01015026; CAG11037.1; -; Genomic_DNA.

InterPro; IPR000290; Ser_thr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

InterPro; PR00069; Pkinase; I.
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SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
NON_TER 1 1 1
NON_TER 483 A8; 54608 MW; 1A970E4D3
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                                                                                   CLARDPARRPSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVL 351
                                                                                                                                                                    EYGDDNVTTAVDIYSFGMCVLEMALLEIHGNGESSYVSQDAINNAIQLLEDPLQKELIQK 293
                                                                                                                                                                                                                                                                                                                                        HGNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPP 232
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AELPRPRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQ
                                                                                                                                                                                                            EYGEVADGTAVDIFSFGMCALEMAVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILC 291
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                                                    CLESDPSVRPTARELLFDPALFEVPLLKLLAAHSIVHHQYMIPENALEEMTKNLDPNLVI
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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           GenCore version 5.1.6 (c) 1993 - 2006 Compugen
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                               SUMMARIES
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Sequence 99, Appl Sequence 10, Appl Sequence 10, Appl Sequence 20, Appl Sequence 32, Appl Sequence 32, Appl Sequence 2, Appli Sequence 2, Appli Sequence 609, App Sequence 270, App Sequence 798, App Sequence 1174, App Sequence 1174, App Sequence 2068, App Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 35, Appl Sequence 37, Appl Sequence 17, Appl Sequence 17, Appl Sequence 108, Appl Sequence 118, Appl S
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US-10-618-941-99
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| US-10-491-467-2 | US-10-052-648A-38 | US-10-437-963-103929 | US-10-425-114-72414 | US-10-424-599-170860 | US-10-114-270-80 | US-10-052-648A-12 | US-10-989-228-40 | US-09-862-027-40 | US-10-196-935A-4 | US-10-052-648A-37 | US-10-478-146-8 | US-10-989-228-34 | US-09-862-027-34 | US-10-052-648A-36 | US-10-460-545-2 | US-10-182-243-50 | US-10-840-512-197 |
| 2 | | Ø | Œ | 1708 | e 80, | | 40, | 40 | Sequence 4, Appli | 37 | 8, 2 | 34, | | 36, | Sequence 2, Appli | 50, , | Sequence 197, App |

ALIGNMENTS

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Sequence 99, Application US/10618941
Publication No. US20040197792A1
GENERAL INFORMATION:
APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: WANNING, GERARD
APPLICANT: CAREEPEEL, SERARD
APPLICANT: CAREEPEEL, SERARD
APPLICANT: CAREEPEEL, SIA
CURRENT FILLING DATE: 034536-0321
CURRENT FILLING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: US/10/618,941
CURRENT FILLING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILLING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOPTWARE: Patentin version 3.2
SEQ ID NO 99
LENGTH: 507
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                            US-10-618-941-99
Query Match 100.0%; Score 2670; DB 4; Best Local Similarity 100.0%; Pred. No. 1.4e-220; Matches 507; Conservative 0; Mismatches 0;
                                                         Length
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Gaps

PSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRP

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APPLICANT: CHARYDCZAK, GLEN
APPLICANT: GRIGORIEV, ICOR
ITITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-1455
CURRENT APPLICATION NUMBER: US/10/840,512
CURRENT FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: 60/469,014
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 185
LENGTH: 499
TYPE: PRT
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US-10-840-512-185
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Best Local Simi
Matches 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CAENEFEEL, SEAN APPLICANT: MANNING, GERARD
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                                                                                                             PMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAPPPEEAQKAKTPTPEP
                                                                                                                                                                                  PSAHNLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAEMPQPHGP
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US-09-862-027-10
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                                                                                                Sequence 10, Application US/10989228
Publication No. US20050089917A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: Novel Kinases and Uses Thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/10/989,228
CURRENT FILING DATE: 2004-11-15
CURRENT FILING DATE: 2004-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020142428A1

GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.

TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FASTSEQ for Windows Version 4.0

1500 NO 10
1500 NO 10
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Best Local Similarity
Matches 301; Conserv
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(326)
OTHER INFORMATION: Xaa = A
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PRIOR APPLICATION NUMBER: US/09/862,027
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.
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Pred. No. 4e-127;
0; Mismatches 2;
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191

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240

245

120

71

60

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; ORGANISM: Homo sapiens
; FEATURE;
; NAME/KEY: VARIANT
; LOCATION; (1)...(326)
; OTHER INFORMATION: Xaa = A
US-10-989-228-10
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Patent No. US20020058264A1
GENERAL INFORMATION:
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Best Local Similarity
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TYPE: PRT
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/840,787
FILING DATE: 23-Apr-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO 10
                                                                                                                                                                                                                                                                                             Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                  CITY: Palo Alto
STATE: CA
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   APPLICATION NUMBER: 09/518,865 FILING DATE: <Unknown>
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Bandman, Olga
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       Sequence 322, Application US/10153668
Publication No. US20030092616A1
GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MURAMATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
PILE REFERENCE: 1254-0207p
                                                                                                                                                     RESULT 6
US-10-153-668-322
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Best Local 9
CURRENT APPLICATION NUMBER: US/10/153,668
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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Similarity 61.6%;
05; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 535 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: BRAITUT03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59;
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Pred. No. 6.5e-123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO:
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102; Indels
           Length
29;
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315 VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME 330 VPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQTLYSQSPALE 270 AVLEIQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFE 137 KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196 77 RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK 17 EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEV-----QKAKTPTPEPFDSETRK VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD AVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE -----APDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEM RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM KTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV--RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK EEEEESEDESEILEESPCGRWQKRREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSE -GLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRK 487 443 427 389 373 329 314 255 163 136 103 76 221 0

Length

29;

Gaps

136

209

149

76

196

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RESULT 7

US-09-764-875-749

Sequence 749, Application US/09764875

Publication No. US20040018969A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Ant FILE REFERENCE: PJZ02

CURRENT APPLICATION NUMBER: US/09/764,875

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or fil
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PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR PELLING DATE: 2001-08-31
PRIOR PELLING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-313175
PRIOR PILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
SEQ ID NO 322
LENGTH: 535
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                                                                                                                                                                                                                                                      QSRLTSLLEETLNKF
                                                                                                                                                                                                                                                                                                                              VVLMQCNI ESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENI PELAAELVQLGF I SEAD
                                                                                                                                                                                                                                                                                                                                                                                                      LDKFLEDVRNGIYPLTAF-----
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61.6%;
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       consult PALM or file wrapper
                                                                                                                                                                                                                                                                                                                                                                                                    -GLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRK
                                                                               Antibodies
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                                                                                                                                                                                      Sequence 2, Application US/10059585
Publication No. US20030082776A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Hayashi, Koji
APPLICANT: Yamamoto, Jun-ichi
APPLICANT: Yamamoto, Jun-ichi
APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Wakamatsu, Ai
 APPLICANT: Yamamoto, Jun-ichi
APPLICANT: Ishii, Shizuko
APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Wakamatsu, Ai
APPLICANT: Wakamatsu, Ai
APPLICANT: Nagai, Keiichi
APPLICANT: Funahashi, Shin-Ichi
APPLICANT: Senoo, Chiaki
APPLICANT: Senoo, Chiaki
APPLICANT: Nezu, Jun-Ichi
APPLICANT: Nezu, Jun-Ichi
APPLICANT: Nezu, Jun-Ichi
APPLICANT: Nezu, Jun-Ichi
APPLICANT: NOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-09801
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
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US-10-059-585-2
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 749
LENGTH: 581
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Best Local Similarity
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVLEIQGNGESSYVPQEAISSAIQLLEDPLQREFIQXCLQSEPARRPTARELLFHPALFE
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Pred. No. 7.26
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7.2e-123;
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487 489 435 373 315

255 267

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Sequence 10, Application US/10040647

Publication No. US20030092154A1

RENERAL INFORMATION:

REPLICANT: (US only) ANTALIS Toni Marie and TITLE OF INVENTION: NOVEL MOLECULES

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESSE: SCULLY, SCOTT, MURPHY & PRESENCES: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: UP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FASEUSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 535
                                                                                                                                                                                                   RESULT 9
US-10-040-647-10
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; ORGANISM: Homo sapiens
US-10-059-585-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFMB
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TELEPAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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FILING DATE: -Unknown
APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
APPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
APPLICATION NUMBER: INternational PC
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,647
PILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID
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TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
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  VVLMQCNIESVEBGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD
                            VIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHEDD
                                                                                                      LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEV-----QKAKTPTPEPFDSETRK
                                                                                                                                                          VPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQTLYSQSPALE
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                                                                                LDKFLEDVRNGIYPLTAF-----GLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRK
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REGISTRATION NUMBER: 31,346
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US-09-925-297-609
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Best Local S
Matches 293
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NUMBER OF SEQ ID NOS: 928
SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 609
LENGTH: 501
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR TITLE TO THE TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TO THE TOTAL T
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OTHER INFORMATION: Xaa equals any
NAME/KEY: SITE
LOCATION: (30)
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NAME/KEY: SITE
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LVHYGFLHEDDRMKLAAFLESTFLKY
                                                                                                                            TPEPFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASE 476
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                                                                                               TPEPAEVETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAE
                                                                                                                                                                                                                           QTLYSQSPALELDKFLEDVRNGIYPLTAF----
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57.9%; Pred. No. 3.6e-115;
Live 64; Mismatches 117;
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PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR RELING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR APPLICATION NUMBER: UP 2001-157043
PRIOR APPLICATION NUMBER: UP 2001-260681
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: UP 2001-313175
PRIOR PRIOR APPLICATION NUMBER: UP 2001-313175
PRIOR PRIOR DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
SOFTWARE: PATENTIN VET: 2.0
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US-10-153-668-434
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Publication No. US20030092616A1
GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 263; Conserv
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APPLICANT: MURAWATSU, Shuji
APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 1254-0207P
CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
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                                         LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSET 425
                                                                                                                              VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME
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                                                                                    VPSLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQTLYSQSPALE
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-GLPRPQQPQQEEVTSPVVP-PLCQDSDT
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RESULT 12 US-11-097-143-270 ; Sequence 270, Application US/11097143 ; Publication No. US20050208558A1

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SOFTWARE: FABLSEQ for Windows Version
SEQ ID NO 270
LENGTH: 637
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-270
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PRIOR PILLING DATE: 1999-10-05
PRIOR PILLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILLING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILLING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILLING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILLING DATE: 2000-03-23
NUMBER OF SEO 1D NOS. 43008
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Best Local Similarity
Matches 245; Conserv
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
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CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
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                                  FLHEDDRMKLAAFLEST 498
                                                                                                          DSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYG
                                                                                                                                                                          QWRYSEVSFME-LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPF
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                                                                      DTESRRI VNMMCSVKI KEDSNDI TMTI LLRMDDKMNRQLTCQVNENDTAADLTSELVRLG
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; Pred. No. 7.4e-92;
77; Mismatches 146;
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EXPRESSION OF
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RESULT 14
US-09-764-875-1053
US-09-764-875-1053
Sequence 1053, Application US/09764875
Publication No. US20040018969A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Prot.
FILE REFERENCE: PJZ02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (307)
; OTHER INFORMATION: X
; NAME/KEY: SITE
; LOCATION: (319)
; OTHER INFORMATION: X
US-09-764-868-798
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 1510
SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 798
LENGTH: 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 798, Application US/09764868 Patent No. US/20020168711A1 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, P.
FILE REFERENCE: PTZ32
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Best Local Similarity
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OTHER INFORMATION: )
NAME/KEY: SITE
(799)
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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NAME/KEY: SITE
LOCATION: (296)
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                                                                                                                                                        VVP-PXVKDFHTXTSLRWRL----
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NUMBER OF SEQ ID NOS: 1249
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1053
LENGTH: 340
                                                                                                                                                                                                                            Sequence 1714, Application US/10292798 Publication No. US20030235833A1 GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABUNATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.4%; Sometive 80.4%; Properties 201; Conservative 29;
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NAME/KEY: SITE
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NAME/KEY: SITE
LOCATION: (296)
OTHER INFORMATION: )
NAME/KEY: SITE
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (307)
OTHER INFORMATION: Xaa equals any of the
NAME/KEY: (315)
LOCATION: (319)
OTHER INFORMATION: Xaa equals any of the
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: SITE
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Pred. No. 1.4e-72;
9; Mismatches 71;
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; NUMBER OF SEQ ID NOS: 2070; SOFTWARE: Patentin Ver. 2:1; SEQ ID NO 1714; SEQ ID NO 1714; LENGTH: 752; TYPE: PRT; ORGANISM: Homo sapiens US-10-292-798-1714
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Best Local Similarity 42.2%; Pred. No. 1.2e-66;
Matches 201; Conservative 39; Mismatches 67
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LMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISE
                                                                               KFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPPEEV-----QKAKTPTPEPFDSETRKVI
                                                                                                                                       SLXLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLABLPR-PRRPPLQWRYSEVSFMELD
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                                                                                                                       SLKLLAAHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQ------
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO1_NEW_PUB.pep:*
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US-10-661-426-7
US-10-70-726-7
US-10-70-726-83
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US-11-109-156-12
US-11-109-156-12
US-11-109-156-12
US-11-109-156-13
US-11-109-156-14
US-11-1004-057-6
US-11-1004-057-6
US-11-004-057-4
US-11-103-055-877-149
US-11-0055-877-149
US-11-113-601-0
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Sequence 1137, Ap
Sequence 7, Appli
Sequence 16, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 183, Appli
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Sequence 19, Appli
Sequence 11, Appli
Sequence 10, Appli
Sequence 10, Appli
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | υ U | 32 | 31 | 30 | 29 | 28 | 27 | 26 | |
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| 127 | 129.5 | 129.5 | 129.5 | 130.5 | 131 | 133.5 | 133.5 | 133.5 | 135.5 | 135.5 | 137 | 138 | 138.5 | 138.5 | 139.5 | 140 | . 140.5 | 140.5 | 142 | |
| 4.8 | 4.9 | 4.9 | 4.9 | 4.9 | 4.9 | 5.0 | 5.0 | 5.0 | 5.1 | 5.1 | 5.1 | 5.2 | 5.2 | 5.2 | 5.2 | 5.2 | 5.3 | 5. W | 5.3 | |
| 1061 | 1306 | 1236 | 418 | 418 | 298 | 1311 | 231 | 231 | 500 | 456 | 656 | 445 | 297 | 297 | 532 | 547 | 970 | 275 | 712 | |
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| US-11-059-814-18 | US-10-995-561-905 | US-11-115-086-4 | US-11-109-156-2 | US-11-099-691-1 | US-10-770-726-51 | US-10-509-422-5 | US-11-151-601-12 | US-11-151-601-5 | US-10-860-501-4 | US-10-860-501-5 | US-10-821-234-1121 | US-10-770-726-70 | US-11-109-156-11 | US-10-770-726-48 | US-10-860-501-7 | US-10-770-726-87 | US-10-770-726-86 | US-10-523-477-10 | US-10-770-726-66 | |
| Sequence 18, Appl | Sequence 905, App | 4 | Sequence 2, Appli | Sequence 1, Appli | 51 | տ | Sequence 12, Appl | Ç, | Sequence 4, Appli | Sequence 5, Appli | | 70, | Sequence 11, Appl | 48, | 7, 2 | 87, | , 98 | | Sequence 66, Appl | |

RESULT 1 US-10-821-234-1137 ALIGNMENTS

Sequence 1137, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Traile REFERENCE: 821A CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07 Treatment 0£ Preeclampsia

NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 137
LENGTH: 588
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1137

Query Match 7.5%; Best Local Similarity 20.6%;

Score 199; DB 6 Pred. No. 7e-10;

DB 6; Length 588;

밁 Ś 밁 ঠ 문 Ś 밁 S 밁 á Best Local Sim Matches 125; 116 TSMDELLKEIQAMSQCHHPNIVSYYTSFVVKDE----LMLVMKLLSGGSVLDIIKHIVAK 230 AF-----LATGGDI-----TRNKVRKTFVGTPCWMAPEVMEQVRGYDFKADIWSFGI 198 IFSNALRPPTALPDDLRSPIRAEREELRNLH-----FFPPEYGEVADG--TAVDIFSFGM 140 KNHKA--MNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHR 197 89 TVFEQLV-----LVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKK--TK 139 69 LPWSINRDDYELQEVIGSGATAVVQAAYCAPKKE---KVAIKRINL------EKCQ 35 GRWQKRR-----EQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQ 9 DPAPRRPTRGCSETIGGGAAAAAAAVGGGETRGEETSEVSEFEGGPRAAAAVMSEDSSA 68 5 EPAPER------ILEESPC CALEMA---GEHKSGVLDESTIATILREVLEGLEYLHKNGQ--IHRDVKAGNILLGEDGSVQIADFGVS 229 Conservative ------VLEIQTNGDTRVTEEAIARARHSLSDPNM------REFI 289 87; Mismatches 213; Indels 182; Gaps 276 171 88 27,

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US-10-661-426-7
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SEQ ID NO 7
LENGTH: 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/661,426
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
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NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sheen, Jen
APPLICANT: Ausubel, Trederick M.
APPLICANT: Asai, Tsuneaki
APPLICANT: Tena, Guillaume
  257
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                                                                                                                                                                                                                                                   111 YGNHEETVRRQICREIEILRDVNHPNVVKCHEMFDQNGE----IQVLLEFMDKGSLE---
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277 TAIELATGAAPYHKYPPMKVLMLTLQNDPPSLETGV-----QDKEMLKKYGKSFRKMI
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                                                                                                                                                                                                                                                                                          ---HEEKIQ----TVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFL 135
                                                                                                                                                                                                                                                                                                                                 SSGSAPSSGGSASSTNTNSSIEAKNYSDLVRGNRIGSGAGGTVYKVIHRPSSRLYALKVI
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GDIWSLGVSILEFYLGRFPFPVSRQGDWASLMCAICMSQPPEAPATASPEFRHFISCCLQ
                                      VDIFSFGMCALEMAV----LEIQTNGDTRVTEEAIARAR----HSLSDPNMREFILCCLA
                                                                                                                                                               -----GAHVWKEQQLADLSRQILSGLAYLH--SRHIVHRDIKPSNLLINSAKNVK
                                                                                                                                                                                                      KKTKKNHKAMNARAWKR-----WCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIK 190
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                                                                                  IADFGVSRILAQDMDPC-----
                                                                                                                      IGSVW-HRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPE-----YGEVADGTA
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                                                                             -NESVGTIAYMSPERINTDLNQGKY-DGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 366;
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Publication No. US20050287569A1
GENERAL INFORMATION:
APPLICANT: Leong, John M.
APPLICANT: Campellone, Kenneth G.
TITLE OF INVENTION: ESPFU NUCLERIC ACIDS AND PROTEINS AND TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 07917-280001
CURRENT APPLICATION NUMBER: US/11/134,563
CURRENT FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: US 60/573,600
PRIOR FILING DATE: 2004-05-20
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US-10-661-426-4
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; ORGANISM: Homo
US-11-134-563-16
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US-11-134-563-16
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SOFTWARE: FASTSEQ for Windows
SEQ ID NO 16
LENGTH: 545
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               APPLICANT: Sheen, Jen
APPLICANT: Ausubel, Frederick M.
APPLICANT: Asai, Tsuneaki
APPLICANT: Tena, Guillaume
TITLE OF INVENTION: Master Activators of Pathogen Responsive
TITLE OF INVENTION: Genes
FILE REFERENCE: 00786/397003
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                                                                                                                                                                                                                                                                                            ---LONPEKLSAIFRDFLNRCLEMDVEKRGSAKELLOHOFL 521
                                                                                                                                                                                                                                                                                                                    RHSLSDPN-----MREFILCCLARDPARRPSAHSLLFHRVL 312
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432

230

386

333

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GENERAL INFORMATION:

APPLICANT: Sheen, Jen

APPLICANT: ABSUBEL, Frederick M.

APPLICANT: ABSUBEL, Frederick M.

APPLICANT: ABSUBEL, Frederick M.

APPLICANT: Tena, Guillaume

ITILE OF INVENTION: Master Activators of Pathogen Responsive

TITLE OF INVENTION: Genes

FILE REFERENCE: 00786/397003

CURRENT FILING DATE: 2003-09-12

FRIOR APPLICATION NUMBER: PCT/US 02/07650

PRIOR FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: US 60/275,199

PRIOR APPLICATION NUMBER: US 60/275,199

PRIOR APPLICATION NUMBER: US 60/275,199

PRIOR FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 366

TYPE: PRI

ORGANISM: Arabidopsis thaliana

US-10-661-426-13
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CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: DOZ/07650
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 4
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US-10-661-426-13
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; ORGANISM: Arabidopsis thaliana
US-10-661-426-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 YGNHEETVRRQICREIEILRDVNHPNVVKCHEMFDQNGE----IQVLLEFMDKGSLE---
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22.3%; Pred. No. 2.2e-09;
ative 54; Mismatches 122;
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CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28

NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patentin version 3.1
SEQ ID NO 131
LENGTH: 524
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1997-11-01
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US-10-878-556A-131
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Matches
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Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: Hoffmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 22.3%;
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                         Local Similarity
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361 A--NQVIHRDIKSDNVLLGMEGSVKLTDFG---FCAQI-----TPEQSKRSTMV
                                     166 ACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELR
                                                                                                            106 HKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLH
                                                                                                                                                          259 --ASGTVFTATDVALGQEVAIKQINL-----QKQPKKELIINEILVMKELKNPNIVN-
                                                                                                                                                                                                                                       201 PVPAPVGDSHVDGAAKSLDKQKKKPKMTDEEIMEKLRTIVSIGDPKKKY-TRYEKIGQG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 GDIWSLGVSILEFYLGRFPFPVSRQGDWASLMCAICMSQPPEAPATASPEFRHFISCCLQ 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 ---HEEKIQ----TVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFL 135
                                                                                                                                                                                                                                                                             4 PEPAP-----RRAREREREREDESEDESDILEE-----SPCGRWQKRREQVNQGN
                                                                           ---FLDSYLVGDELFVVMEYLAGGSLTDVVTET----CMDEAQIAAVCRECLQALEFLH
                                                                                                                                                                                                MPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVL---VDHPNIVKL 105
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                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                  6.9%; Score 184.5; DB 6;
23.3%; Pred. No. 1.1e-08;
htive 60; Mismatches 126;
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Pred. No. 2.2e-09;
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US-10-661-426-12

Sequence 12, Application US/10661426

Publication No. US20050262584A1

GENERAL INFORMATION:
APPLICANT: Sheen, Jen
APPLICANT: Augubel, Frederick M.
APPLICANT: ABBAI, TBuneaki
APPLICANT: Tena, Guillaume
TITLE OF INVENTION: Master Activators of Pathogen Res
TITLE OF INVENTION: Genes
FILE REFERENCE: 00786/397003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AMIG1079 (031896-01000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PatentIn version 3.2
SEQ ID NO 71
SEQ ID NO 71
                                                                                                                                                                                                                                                                                                           RESULT 8
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US-10-770-726-71
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Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
  CURRENT APPLICATION NUMBER: US/10/661,426
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                                                                                                                                                                                                                                                                                                                                                                                                                       283 ----PNMREFILCCLARDPARRPSAHSLLFHRVL 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 GSTGIVCIATVRSSGKLVAVKKMDLRKQQRRELLFNEVVIMRDYQHENVVEMYNSYLVGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AAPEPAPRRAREREREREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAM-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELISRLPYGPEVDIWSLGIMVIEM-----VDGEPPYFNEPPLKAMKMIRDNLPPRLKNL
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PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 348
TYPE: PRT
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US-10-523-477-11
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US-10-661-426-12
                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-523-477-11
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
LENGTH: 403
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/10523477 Publication No. US20050266406A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MAXS AS MODIFIERS OF THE AXIN PATHWAY AND METHODS OF USE FILE REFERENCE: EX03-051C-US CURRENT EAPLICATION NUMBER: US/10/523,477 CURRENT FILING DATE: 2005-02-04 PRIOR APPLICATION NUMBER: US 60/401,534 PRIOR APPLICATION NUMBER: US 60/401,534 PRIOR PILING DATE: 2002-08-07 PRIOR PILING DATE: 2002-08-07 PRIOR PILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: EXELIXIS, INC
                                                                                                                                                                                                                                                                             Match 6.3%;
Local Similarity 24.0%;
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                                                                                                                                                    104 SAPENNP----EEBLASKQKNEESKKRQWALEDFEIGR-----PLGKGK----FGNVYLA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 RVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKR-----WCTQILSALSFLHACSPPII 172
119 VIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTS 178
                                               151 REKQSKFILALKVL-FKAQLEKAGVEHQLRREVEIQSHLRHPNILRLYGYFHDAT----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 VWNELHFGDRKAFAA-----HEEKIQ----TVFEQLVLVDHPNIVKLHKYWLDTSEACA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 VYKVIHTPTSRPFALKVIYGNHEDTVRRQICREIEILRSVDHPNVVKCH----DMFDHNG 139
                                                                                                                                                                                                                                                        76;
                                                                                                                                                                                                   2 AAPEPAPRRARERE---REREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLA 58
                                                                                                 MDTEEGVEVVWNEIHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACAR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APATASQEFRHFVSCCLQSDPPKRWSAQQLLQH
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Pred. No. 2e-07;
1; Mismatches 131;
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FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 83
LENGTH: 403
TYPE: PRT
      RESULT 11
US-10-770-726-85
; Sequence 85, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
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US-10-770-726-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo
-10-770-726-83
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APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCERS
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wyeth
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                                                                                                                                LKHNPSQRPMLREVLEH 380
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                                                                                                                                                                                                                                                                                                      VYLILEYAPLGTVYRELOKLSKFDEQRTA----TYITELANALSYCH--SKRVIHRDIKP
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Brown, Eugene
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US-11-109-
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APPLICANT:
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APPLICANT:
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; ORGANISM: Homo sapiens
US-10-770-726-85
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SEQ ID NO 85
LENGTH: 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
                                            293 LARDPARRPSAHSLLFH 309
                                                                                                                                  237 VADGTAVDIFSFGMCALEMAVLEIQTNGDT-RVTEEAIARARHSLSD---PNMREFILCC
                                                                                                                                                                                                                                                                                                                                                                               151 REKOSKFILALKVI-FKAQLEKAGVEHQLRREVEIQSHLRHPNILRLYGYFHDAT----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 SAPENNP----EEELASKOKNEESKKROWALEDFEIGR-----PLGKGK---FGNVYLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
76; Conserv
LKHNPSQRPMLREVLEH 380
                                                                                        MHD-EKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLISRL
                                                                                                                                                                                      ENLLLGSAGELKIAD----FGWSVHAPSSRRTTL-
                                                                                                                                                                                                                                   DTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEY--GE
                                                                                                                                                                                                                                                                                  VYLILEYAPLGTVYRELOKLSKFDEORTA----TYITELANALSYCH--SKRVIHRDIKP
                                                                                                                                                                                                                                                                                                               VIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTS
                                                                                                                                                                                                                                                                                                                                                                                                                            MDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACAR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.3%;
ilarity 24.0%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 168.5; DE; Pred. No. 2e-07; 61; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                      -CGTLDYLPPEMIEGR
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SSULT 12
S-11-109-156-12
Sequence 12, Application US/11109156
Publication No. US20050250144A1
GENERAL INFORMATION:
APPLICANT: Toshio Ota
APPLICANT: Toshio Ota
APPLICANT: Tetsuo Nishikawa
APPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
APPLICANT: Koji Hayashi
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Tetsuji Otsuki
APPLICANT: Chiaki Senoo
APPLICANT: Oun-Ichi Punahashi
APPLICANT: Oun-Ichi Punahashi
APPLICANT: Oun-Ichi Wezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION NOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION NOVEL GENES ENCODING PROTEIN
TITLE OF THE DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 1999-10-18

KINASE/PROTEIN

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PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR PELICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 12
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US-11-092-168-1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-12
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/11092168 Publication No. US20050277658A1
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Best Local :
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APPLICANT:
APPLICANT:
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                                                     TITLE OF INVENTION: PROTEIN KINASE INHIBITORS FILE REFERENCE: 920214.00003CONT3 CURRENT APPLICATION NUMBER: US/11/092,168 CURRENT FILING DATE: 2005-03-29 PRIOR APPLICATION NUMBER: US 10/965,313
                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Arizona Board of Regents on behalf of The University of Arizona APPLICANT: Montigen Pharmaceuticals, Inc.
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$ 60/608,529
$ 60/511,486
$ 60/511,489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/183,322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 VIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTS
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                                                                                                                                                   Warner, Steven L.
Della Croce, Kimiko
Von Hoff, Daniel D.
Grand, Cory L.
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                                                                                                                                                                                                                                               Bearss, David J.
Vankayalapati, Hariprasad
Bashyam, Sridevi
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Pred. No. 2e-07;
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US-10-661-426-9
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                                                                                                                     ORGANISM: Arabidopsis thaliana
US-10-661-426-9
                                                                                                                                                    ; SEQ ID NO 9
; LENGTH: 348
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10661426 Publication No. US20050262584A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 76; Conserv
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                      Best
                                                    Matches
                                                                                    Query Match
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Master Activators of Pathogen
TITLE OF INVENTION: Genes
FILE REFERENCE: 00786/397003
CURRENT APPLICATION NUMBER: US/10/661,426
CURRENT FILLING DATE: 2003-09-12
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
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TYPE: PRT
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                                                                    Local
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66;
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                                                  h 6.3%;
Similarity 24.2%;
66; Conservative 39
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Tena, Guillaume
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                                                  Score 167.5; DI
Pred. No. 2e-07
39; Mismatches
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Pred. No. 2e-(
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                                                  103; Indels 65;
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                                                  Gaps
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RESULT 15

US-10-661-426-14

/ Sequence 14, Application US/10661426

/ Publication No. US20050262584A1

/ GENERAL INFORMATION:
Search completed: January 12, 2006, 11:33:39 Job time : 32 secs
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SOFTWARE: FABTSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-661-426-14
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APPLICANT: Tena, Guillaume
TITLE OF INVENTION: Master Activators of Pathogen Responsive
FILE REFERENCE: 00786/397003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/661,426
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
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                                                                                     290
                                                                                                               278 -HSLSDPNMREFILCCLARDPARRPSAHSLLFH 309
                                                                                                                                                                          231 PERINTDLNHGRY-DGYAGDVWSLGVSILEFYLGRPPFAVSRQGDWASLMCAICMSQPPE 289
                                                                                                                                                                                                                   232 PE-----YGEVADGTAVDIFSFGMCALEMAV----LEIQTNGDTRVTEEAIARAR---
                                                                                                                                                                                                                                                                185 HRDIKPSNLLINSAKNVKIADFGVSRILAQTMDPCNS------SVGTIAYMS 230
                                                                                                                                                                                                                                                                                                        173 HGNLTSDTIFIQHNGLIKIGSVW-HRIFSNALRPTALPDDLRSPIRAEREELRNLHFFP 231
                                                                                                                                                                                                                                                                                                                                                          140 EIQVLLEFMDQGSLE------GAHIWQEQELADLSRQILSGLAYLH--RRHIV 184
                                                                                                                                                                                                                                                                                                                                                                                                    118 RVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKR-----WCTQILSALSFLHACSPPII 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 HRDIKPSNLLINSAKNVKIADFGVSRILAQTMDPCNS-----SVGTIAYMS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 EIQVILEFMDQGSLE------GAHIWQEQELADLSRQILSGLAYLH--RRHIV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 PERINTDLNHGRY-DGYAGDVWSLGVSILEFYLGRFPFAVSRQGDWASLMCAICMSQPPE 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 APATASQEFRHÉVSCCLQSDÉPKRWSAQQLLQH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 VYKVIHTPTSRPFALKVIYGNHEDTVRRQICREIEILRSVDHENVVKCH----DMFDHNG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 VWNELHFGDRKAFAA-----HEEKIQ----TVFEQLVLVDHPNIVKLHKYWLDTSEACA 117
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                                                                                  APATASQEFRHFVSCCLQSDPPKRWSAQQLLQH 322
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Asai, Tsuneaki
Tena, Guillaume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -HSLSDPNMREFILCCLARDPARRPSAHSLLFH 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PE----YGEVADGTAVDIFSFGMCALEMAV----LEIQTNGDTRVTEEAIARAR--- 277
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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -WODEL=frame+ D2n.model -DEV=xlp
-WODEL=frame+ D2n.model -DEV=xlp
-WODEL=frame+ D2n.model -DEV=xlp
-WODEL=frame+ D2n.model -DEV=xlp
-CQ-/CGP12 1/USFTO spool p/US10618941/runat 12012006 070207 14416/app_query.fasta_1.647
-CQ-/CGP21 - DEP_D11catIons NA New -QFWT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=blue -STRAT=1 -END=-1 -MATRIX=bluesum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US10618941 @CGN 11 184 @runat 12012006 070207_14416
-NCTU=6 -ICPU=3 -NO MMAP -LARGROUTERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
-MODEL=frame+_p2n.model
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         383.5
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Ygapop 10.0, Y
Fgapop 6.0, F
Delop 6.0, I
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
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Ygapext
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US-11-128-061-2970

US-11-128-061-6612

US-10-623-155-23

US-10-955-054A-44

US-11-136-527-688

US-11-136-527-688

US-10-770-726-27

US-10-821-234-285

US-10-661-426-6
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                 Sequence 2970, Ap
Sequence 6612, Ap
Sequence 23, Appl
Sequence 44, Appl
Sequence 688, Appl
Sequence 27, Appl
Sequence 285, Appl
Sequence 285, Appl
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  Appli
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ALIGNMENTS

RESULT 1 US-11-128-061-2970

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Hann, Louane E.

APPLICANT: Sinacore, Markin S.

APPLICANT: Brown, Eugene L.

APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: MONITOR GENE EXPRESSION

FILE REFERENCE: 01997.027701

CURRENT APPLICATION NUMBER: US/11/128,061

CURRENT APPLICATION NUMBER: US/11/128,061

CURRENT APPLICATION NUMBER: US/11/128,061

PRIOR APPLICATION NUMBER: US/11/128,061

PRIOR FILING DATE: 2005-05-11

NUMBER OF SEQ ID NOS: 7285

SOFTWARE: Patentin version 3.3

SEQ ID NO 2970

LENGTH: 540

TYPE: DN*
                                                    Alignment Scores:
                                                                                           US-11-128-061-2970
 Percent Similarity:
                                     Pred. No.:
8.22e-37
413.00
81.82%
                  Length:
Matches:
 Conservative:
540
74
16
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APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLI
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT APPLICATION NUMBER: US 60/570,425
PRIOR APPLICATION WEBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
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DB:
                                                                                                    US-10-618-941-99 (1-507) x US-11-128-061-6612 (1-540)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
                                                                                                                                                                                                                                                                                          SEQ ID NO 6612
LENGTH: 540
TYPE: DNA
ORGANISM: Cricetulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6612, Application US/11128061 Publication No. US20060003958A1
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.3
                                                                                                                                                                       Local Similarity:
                                                                                                                                                                                                                           No.:
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                                   211 GAGGAGGAAGAAAGTGAAGATGAGTCTGAGATCTTGGAAGAGTCCCCCCTGTGGACGC
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 TrpGlnLysArgArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPhe
                                                     GluArgGluAspGluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArg
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CURRENT APPLICATION NUMBER: US/10/623,155;
CURRENT FILING DATE: 2003-07-17;
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FASESEQ for Windows Version 4.0;
SEQ ID NO 23;
LENGTH: 669
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 642, 661;
OTHER INFORMATION: n = A,T,C or G
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; Sequence 23, Application US/10623155
; Publication No. US20050261166A1
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Tongtong
APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: FURNITION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C20
                                                   169
                                                                                                               127
                                                                                                                                                                                                                                                              349 AlaValleuAlaGluLeuProArg---ProArgArgProProLeuGlnTrpArgTyrSer 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
                    422
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AspSerGluThrArgLysValIleGlnMetGlnCysAsnLeuGluArgSerGluAspLys
                                                 GAGGAGGTGACATCACCTGTCGTGCCCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCT
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APPLICANT: SYMMANS, W. FRASER
APPLICANT: HESS, KENNETH R.
APPLICANT: HESS, KENNETH R.
APPLICANT: AYERS, MARK
APPLICANT: STEC, JAMES
TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
FILE REFERENCE: UTXC:8880US
CURRENT APPLICATION NUMBER: US/10/955,054A
CURRENT APPLICATION NUMBER: US/10/955,054A
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin Ver. 2.1
150CTM. 6813
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TYPE: DNA
ORGANISM: Homo sapiens
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                   GluAlaCysAlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGln 133
                                                                                                                                                                       PheGlyAspArgLysAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGln
                                                                                                                                                                                                                               SerThrPheLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHis
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AAAGGAAAGAAGTGCATTGTTTGGTGACTGAACTTATGACGTCTGGAACACTTAAAACG
                                                                THAMAGETETTCAGCATCCCAATAITGTTAGATTTTATGATTCCTGGGAATCCACAGTA 671
                                                                                                                                                                                                         ACGGTCTACAAAGGTCTGGACACTGAAACCACCGTGGAAGTCGCCTGGTGTGAACTGCAG
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                                                                                                 LeuValLeuValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSer 113
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                                                                                                                                                                          AspSerGluThrArgLysValIleGlnMetGlnCysAsnLeuGluArgSerGluAspLys
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                              TyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGly 481
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                                                                                                                                               -----AAAGATAATGAAGCTATTGAGTTTTCTTTTTGATTTÄGÄGÄGÄ-
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                GATGTCCCAGAAGATGTTGCACAAGAAATGGTAGAGTCTGGG
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APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: Probe Arrays For Expression Profiling of I
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 688
LENGTH: 7555
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-688
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Publication No. US20050287570A1
GENERAL INFORMATION:
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No.:
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                                                AGCTGGTGTCGGCAAATCCTTAAAGGACTTCAATTTCTCCATACACGAACTCCCCGATT
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IleHisGlyAsnLeuThrSerAspThrIlePheIleGln---HisAsnGlyLeuIleLys
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                                                                            ArgTrpCysThrGlnIleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIle 171
                                                                                                            AAAACGTACTTAAAAAGG------TTTAAAGTGATGAAAATCAAAGTTTTAAGA
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Sequence 27, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
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; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 2838
; TYEE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27
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Best Local Similarity:
Query Match:
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                                                           GCCCAGGTGAGCAAGGAAGTGCCC--
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FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR TILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 285
LENGTH: 4529
TYPE: DNA
ORGANISM: Homo sapiens
US-10-821-234-285
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 285, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
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APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and
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APPLICANT: Stache-Crain, Birgit
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| Qy 197 ArgIlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro 216 B46 TGCTTTTTAGCAACTG-GTGGTGATATTACCCGAA | Qy 122 IleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLys 139 Comparison of the content of the cont | Qy 35 GlyArgTrpGlnLy8ArgArg | Alignment Scores: Pred. No.: 199.00 Matches: 131 Conservative: 88 Best Local Similarity: 21.72% Ouery Match: 7.45% DB: Wismatches: 211 Ouery Match: 7.45% DB: US-10-618-941-99 (1-507) x US-10-821-234-285 (1-4529) Qy 5 GluProAlaProArgArg |
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| Oy 494 PheLeuGiu 496 Db 1795 AATTTGCAG 1803 RESULT 8 US-10-661-426-6 ; Sequence 6, Application US/10661426 ; Publication No. US20050262584A1 ; GENERAL INFORMATION: ; APPLICANT: Ansubel, Frederick M. ; APPLICANT: Ausubel, Frederick M. ; APPLICANT: Tena, Guillaume ; TITLE OF INVENTION: Master Activators of Pathogen Responsive ; TITLE OF INVENTION: Genes | 156 43 167 167 | 1291 364 1345 383 383 391 1456 411 | 1000 TTGGCTACAGGGGCGCTCCTTATCATAAATATCCACCAATGAAGGTTTTAATGCTGACA 262 ThrasnGlyaspThrargValThrGluGluAlaIleAlaargAlaargHisSerLeuSer 1060 CTGCAGAACGATCCTCCTTCTTTGGAAACTGTGTT- 282 AspProAsnMet |

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FILE REFERENCE: 00786/397003
CURRENT APPLICATION NUMBER: US/10/661,426
CURRENT APPLICATION NUMBER: DOZ/07650
PRIOR APPLICATION NUMBER: PCT/US 02/07650
PRIOR PILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,199
PRIOR FILING DATE: 2001-03-12
NUMBER: OF SEQ ID NOS: 16
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 6
ELENCTH: 1101
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-661-426-6
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Best Local Similarity:
Query Match:
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                                                                                                                                                IleGlySerValTrp---HisArgIlePheSerAsnAlaLeuArgProProThrAlaLeu
                                                                                                                                                                                                        IleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLys 190
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                                                                                       ProAspAspLeuArgSerProIleArgAlaGluArgGluGluLeuArgAsnLeuHisPhe
                                                                                                                      ATTGCTGATTTTGGAGTTAGTÄGGATCTTGGCTCAGGATATGGATCCGTGT-----
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LENGTH: 1400
TYPE: DNA
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US-10-618-941-99 (1-507) x US-11-136-527-6476 (1-1400)
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Publication No. US20050287570A1
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101066)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                      40 gArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPheLeuAlaMetAs
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                      eAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuVal-----
                                                                             TGTAGCCACAGGGCAGGAGGTGGCCATTAAACAGATGAACCTT-
                                                                                                                             pThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAspArgLysAlaPh
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APPLICANT: Leong, John M.

APPLICANT: Campellone, Kenneth G.

APPLICANT: Campellone, Kenneth G.

TITLE OF INVENTION: ESPFU NUCLEIC ACIDS AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 07917-280001

CURRENT APPLICATION NUMBER: US/11/134,563

CURRENT FILING DATE: 2005-05-20

PRIOR APPLICATION NUMBER: US 60/573,600

PRIOR APPLICATION NUMBER: US 60/573,600

PRIOR FILING DATE: 2004-05-20

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FRSESEQ for Windows Version 4.0

SEQ ID NO 15

LENGTH: 1638
Alignment Scores:
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                       -----CTTCAGAACCCAGAGAAGCTGTCAGCTATCTTCCGGGACTTTCTGAA 1496
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APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
ITILE OF INVENTION: Probe Arrays For Expression Pro
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: 06/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 2389
LENGTH: 2539
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                                                 GACAGAAACC--
                                                                           uLysLysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysTh 155
                                                                                                            GGGAGATGAGCTATGGGTTGTCATGGAATACTTGGCCGGAGGCTCCTTAACAGATGTGGT 1452
                                                                                                                                                                                               -----AspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAl 115
                                                                                                                                                                                                                                                                     sAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuVal-- 97
                                                                                                                                                                                                                                                                                                                               aMetAspThrGluGluGlyValGluValValTrpAsnGluLeuH1sPheGlyAspArgLy
                                                                                                                                           aCysAlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLe 135
                                                                                                                                                                          GGAAAACAAAAACCCAAACATTGTGAAC-----TATCTGGACAGTTACCTTGT 1392
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US-10-618-941-99 (1-507) x US-10-661-426-3 (1-1101)
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Master Activators of Pathogen Responsive TITLE OF INVENTION: Genes FILE REPERENCE: 00786/197003

CURRENT APPLICATION NUMBER: US/10/661,426

CURRENT FILING DATE: 2003-09-12

PRIOR APPLICATION NUMBER: PCT/US 02/07650

PRIOR PILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: US 60/275,199

PRIOR PILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ausubel, Frederick M. APPLICANT: Asai, Tsuneaki APPLICANT: Tena, Guillaume
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                                                                                          GCAAGTCCGAGCCAGAACAGGTCT---CCTCAGAATCTACATCAACTCTTGCCTCCT---
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Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
FILE REFERENCE: 031996-041000 (AM101086)

FILE REFERENCE: 031996-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT PILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 3130
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/ ORGANISM: Rattus
US-11-136-527-3130
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US-11-136-527-3130
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AsnGlyLeuIleLysIleGlySerValTrpHisArgIlePheSerAsnAlaLeuArgPro
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                                                    GCT-----AATCAAGTGATCCACAGAGACATCAAAAGTGACAATGTGCTTTTGGGAATG
                                                                                       AlaCysSerProProIleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHis
                                                                                                                          GATGAAGCGCAGATCGCAGCTGTGCAGAGAGTGTTTACAGCCGTTGGAGTTTTTACAT
                                                                                                                                                            AsnAlaArgAlaTrpLysArgTrpCysThrGlnIleLeuSerAlaLeuSerPheLeuHis 165
                                                                                                                                                                                                                                                                                                          HisLysTyrTrpLeuAspThrSerGluAlaCysAlaArgValIlePheIleThrGluTyr 125
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APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031895-041000 (AM101086)

FILE REFERENCE: 031895-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 2475

LENGTH: 2241

Type: DNA

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US-11-136-527-2475
; Sequence 2475, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
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APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 39
LENGTH: 2253
                                                                                                                                                                                                                                                                               RESULT 15
US-10-770-726-39
; Sequence 39, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
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Search completed: January 14, 2006, 03:09:55 Job time : 407 secs

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Regult
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MXX=100
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1: /cgn2_6/ptodate/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodate/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodate/1/pubpna/US08_PUBCOMB.seq:*

4: /cgn2_6/ptodate/1/pubpna/US08_PUBCOMB.seq:*

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Fgapop 6.0 , Fgapext
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US-10-425-114-26870

US-10-425-114-26848

US-10-425-114-26873

US-10-425-114-28974

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US-10-175-523-117
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Sequence 33, Appl
Sequence 26870, A
Sequence 26848, A
Sequence 26873, A
Sequence 28974, A
Sequence 71, Appl
Sequence 117, App
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; Sequence 33, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
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| US-10-490-592-6 US-10-490-592-4 | 10-400-501-6 | -10-433-794-3 | -353-929-5 | -10-017-161-2 | -09-764-875-1 | -09-764-868- | -10-292-798-1 | 9-814-353- | -09-814- | -353- | -10-104-047- | -09-814-353-2 | -006-285-2 | -764-875-15 | -764-868-20 | -006-285-456 | 1-060-756-44 | 50-756-44 | 1-060-756-14 | 1-060-756- | -956-157-70 | -09-764-875- | 09-764-868-18 | S-11-097-143 - 26 | S-11-097-143- | 09-925-297-15 | -10-040-647-9 | -10-153-668- | -10-059-585- | -09-764-875- | -10-956-157-18 | -10-887-553A-88 | -10-153-668-32 | -09-840-787-6 | -10-989-22 | -09-862-027- |
| Sequence 6, Appli Sequence 4, Appli | ٠. | 37. Ac | e 58, Ap | 2067, | æ | 1369, | 1713, | Sequence 8052, Ap | 1699, | | 1939, A | 2000 | 280, Ap | 152, | 209 | equence 456, App | equence 4413, | e 44 | equence 141 | ce 14 | equence 7080 | equence 455, | _ | æ | 6 | e L | φ | 4 | equence 1 | equence 1 | equence 1 | equence 8 | e u | equence 6 | equence 9 | equence |

ALIGNMENTS

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US-10-618-941-99 (1-507) x US-10-618-941-33 (1-3765
                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                               Score:
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                                                                                                          US-10-618-941-33
                                                                                                                 SEQ ID NO 33
LENGTH: 3765
TYPE: DNA
ORGANISM: Homo sapiens
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2670.00
100.00%
100.00%
                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                     3765
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CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15

NUMBER OF SEQ ID NOS: 143 SOFTWARE: PatentIn version 3.2

APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAENEPEEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321

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                                                                                    ThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMetAlaValLeuGluIle
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ProLeuGlnTrpArgTyrSerGluValSerPheMetGluLeuAspLysPheLeuGluAsp
                               AAGACCAAGGCCATGGACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGCAGGCCC
                                               LysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeuProArgProArgArgPro
                                                                                                                                                                ProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValHisSerLeuLysLeu
                                                                                                                                                                                                           AGTGACCCCAACATGCGGGAGTTCATCCTTTGCTGCCTGGCCCGGGACCCTGCCCGCCGG
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Sequence 26870, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 26870

LENGTH: 3837

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

COURTEST INFORMATION: Close ID: LIBASES-003-617 FILI
                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-425-114-26870
                                                                                                                                                                    US-10-618-941-99 (1-507) x US-10-425-114-26870 (1-3837)
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                      GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg 40
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GAGAGCGAGGACGAGACATCCTGGAGGAAAGCCCCGTGTGGTCGCTGGCAAAAGCGA
                                                                                                      GlyPheLeuHisGluAspAspArgMetLysLeuAlaAlaPheLeuGluSerThrPheLeu 500
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AAGCTCCTGGCAGCCCACTGCTTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTG
                                                                   ArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGluValHisSerLeu
                                                                                                                             SerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAlaArgAspProAla
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APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack B

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT TILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 26848

LENGTH: 3838

TYPE: PN''
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Score:
                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                      US-10-618-941-99 (1-507)
                                                                                                                                                              ; OTHER INFORMATION: US-10-425-114-26848
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US-10-425-114-26848
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ORGANISM: Homo :
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                                                                                                                                                                        Clone ID: LIB4654-015-F10_FLI
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                                                              APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28974
LENGUTH: 3128
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
Alignment Scores: Pred. No.:
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Sequence 71, Application US/10840512
Publication No. US20050125852A1
GENERAL INFORMATION:
APPLICANT: CAENEPEEL, SEAN
APPLICANT: MANNING, GERARD
APPLICANT: CHARYDCZAK, GIEN
APPLICANT: CHARYDCZAK, GIEN
APPLICANT: GRIGORIEV, IGOR
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-1455
CURRENT APPLICATION NUMBER: US/10/840,512
CURRENT FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: 60/469,014
PRIOR PILING DATE: 2003-05-09
SUMMER OF SEQ ID NOS: 239
SOFTWARE: Patentin version 3.2
SEQ ID NO 71
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RESULT 7

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US-10-175-523-117

Sequence 117, Application US/10175523

Publication No. US20030096264A1

GENERAL INFORMATION:

APPLICANT: Evans, David

APPLICANT: Evans, David

APPLICANT: Hook, Derek

APPLICANT: Klimczak, Leszek

APPLICANT: MILTENWAN, Michael

APPLICANT: MAIGNER, PASCA1

APPLICANT: RAJAN, Prithi

TITLE OF INVENTION: MULTI-DARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)

FILE REFERENCE: 3235/10795-US3

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US 60/299,151

PRIOR APPLICATION NUMBER: US 60/317,828

PRIOR PILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: US 60/325,150

PRIOR APPLICATION NUMBER: US 60/325,150

PRIOR APPLICATION NUMBER: US 60/333,047

PRIOR APPLICATION NUMBER: US 60/333,047

PRIOR APPLICATION NUMBER: US 60/339,936

PRIOR PILING DATE: 2001-10-25

PRIOR APPLICATION NUMBER: US 60/349,936

PRIOR APPLICATION NUMBER: US 60/349,936

PRIOR PILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: US 60/349,936

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; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 3538
; TYPE: DNA
; ORGANISM: Homo sapiens
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                                      ArgAlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGluVa1
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US-11-099-266-117
; Sequence 117, Application US/11099266
; Publication No. US20050181433A1
; GENERAL INFORMATION:
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APPLICANT: Evans, David
APPLICANT: Hook, Derek
APPLICANT: Klimczak, Leszek
APPLICANT: Laeng, Pascal
APPLICANT: Palfreyman, Michae
APPLICANT: Laeng, Pascal
APPLICANT: Palfreyman, Michael
APPLICANT: Palfreyman, Michael
APPLICANT: Rajan, Prithi
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS
FILE REFERENCE: 03235/100J795-US4
CURRENT APPLICATION NUMBER: US/11/099,266
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: US 10/175,523
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,151
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PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR APPLICATION NUMBER: US 60/361,834
PRIOR APPLICATION NUMBER: US 60/361,834
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PAtentin version 3.1
SEQ ID NO 117
LENGTH: 3538
TYPE: DNA
ORGANISM: Homo sapiens
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Query Match:
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                                               LeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThr
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 AGCGACACCATCTTCATTCAGCACAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGA
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Matches:
Conservative:
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RESULT 9
US-09-862-027-9
; Sequence 9, Application US/09862027
; Patent No. US20020142428A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. US20020142428A1el Kinases
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
                                                                                                                                                                                                                                                                                                                          ThrPheLeuLysTyrArgGlyThrGlnAla
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PRIOR APPLICATION NUMBER: US 09/345,47
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 981
TYPE: DNA
ORGANISM: Homo &
FEATURE:
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LOCATION: (1)...(981)
OTHER INFORMATION: n=A,T,C
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                                                                                                 LeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeuThrSerAspThr
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CGAGAGGAACTTCGGAACCTGCACTTCTTCCCCCCCAGAGTATGGAGAGGTGGCCGATGGG
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Matches:
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APPLICANT: Hodge, Martin R.
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: Novel Kinases and Uses The
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/10/989,228
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US/09/862,027
PRIOR FILING DATE: 2001-05-21
PRIOR PRILING DATE: 1909-06-30
NUMBER OF SEO ID NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEO ID NOS: 82
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 981
TYPE: DNA
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Best Local Similarity:
Query Match:
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US-10-989-228-9
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Publication No. US20050089917A1
GENERAL INFORMATION:
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Patent No. US20020058264A1
GENERAL INFORMATION:
                                                                               Yue, Henry
Guegler, Karl J.
CORLEY, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
RUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lal, Preeti
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    CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
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Bandman, Olga
Shah, Purvi
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INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
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LIBRARY: BRAITUT03
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MEDIUM TYPE: Diskette
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                     IleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeu
                                                                                                         LyeThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln
                                                                                                                                                                GCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAAG
                                                                                                                                                                                      AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys
                                                                                                                                                                                                                                                                           ValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCys 116
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCTG
                                                                                 AAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACAA
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ArgMetLysLeuAlaAlaPheLeuGluSerThrPheLeuLysTyr
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APPLICANT: MATSUDA, Akio
APPLICANT: MATSUDA, Akio
APPLICANT: MATSUDA, Akio
APPLICANT: MATSUDA, Shuji
APPLICANT: MIRAMATSU, Shuji
APPLICANT: ISHIZAMA, Kenya
FILE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
CURRENT FILING DATE: 2002-05-24
PRIOR PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR FILING DATE: 2001-08-31
PRIOR PRIOR PILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-313175
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; LOCATION: (113)..
US-10-153-668-321
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Query Match:
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                        IleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeu
                                                                                                                         LysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln
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ATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCTG
                                                                                              AAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACAA
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RESULT 12
US-10-153-668-321
; Sequence 321, Application US/10153668
; Publication No. US20030092616A1

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RESULT 13
US-10-887-553A-882
; Sequence 882, Application US/10887553A
; Publication No. US20050085436A1
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                                                                                  CAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTC 1666
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APPLICANT: Li, Hao

TITLE OF INVENTION: wethod to treat conditions associated

TITLE OF INVENTION: with insulin signalling dysregulation

FILE REFERENCE: 4-33262

CURRENT APPLICATION NUMBER: US/10/887,553A

CURRENT FILING DATE: 2004-07-08

PRIOR APPLICATION NUMBER: 60/485,883

PRIOR APPLICATION NUMBER: 60/485,883

PRIOR APPLICATION NUMBER: 60/485,883

PRIOR FILING DATE: 2003-08-07

NUMBER OF SEQ ID NOS: 1208

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 882

LENGTH: 2163

TYPE: DNA

ORGANISM: human

ORGANISM: human
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   ValAlaAsp---GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet 255
                                                                                                                           ArgIlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro
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RESULT 14
US-10-956-157-1845
(S-10-956-157-1845); Sequence 1845, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
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APPLICANT: Wyeth
APPLICANT: Weth
APPLICANT: Wounts, William
APPLICANT: MOUNTS, WILLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED |
TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2041-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 1845
LEEGTH: 2163
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                          GAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGAC
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                                                                                                                                                                                                                                                                                                                                                                              CTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAAT 156:
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                                                                                                                                          AlaValLeuGluIleGlmThrAsmGlyAspThrArg---ValThrGluGluAlaIleAla 274
       ValHisSerLeuLysLeuLeuAlaAlaHisCysPheIleGlnHisGlnTyrLeuMetPro 334
                                 TCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTTCCACCCAGCATTGTTTGAA 1099
                                                                                      ArgAspProAlaArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGlu 314
                                                                                                               ArgAlaArgHisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAla 294
                                                                                                                                                                                                ValAlaAsp---GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet 255
                                                                                                                                                                                                                                                       GTGAAGACTTGTCGAGAAGAAGAAGAATCTACACTTCTTTGCACCAGAGTATGGAGAA
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| 37 TrpGlnLysArgArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPhe | 17 GluargGluaepGluSerGluhepGluSerAepI | 57.47% Indele: 3 Gape: 7) x US-09-764-875-151 (1-2225) | Pred. No.: 2.61e-175 Length: 2225 Score: 1534.50 Mismatches: 305 Best Local Similarity: 73.54% Conservative: 59 Best Local Similarity: 61.62% Mismatches: 102 | | SEQ ID NO 151 LENGTH: 2225 TYPE: DNA ORGANISM: Homo sapiens | CURRENT FILING DATE: 2001-01-17 Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1249 SOFTWARE: PATENTIN VER. 2.0 | APPLICANT: ROSEN et al. TITLE OF INVENTION: Nucleic FILE REFERENCE: PJZ02 CURRENT APPLICATION NIMBER: | RESULT 15 US-09-764-875-151 ; Sequence 151, Application US/09764875 ; Publication No. US20040018969A1 ; GENERAL INFORMATION: | QY 488 ATGMEtLysLeuAlaAlaPheLeuGluSerThrPheLeuLysTyr 502 | 1562 | 150 CTTCTGCTGAAGTTGGAGACAAACTGAACCGGACCTGAGCTGTGACCTGAAGTAAAT | 428 ValileGlimMetGlinCysAsnLeuGluArgSerGluAspLysAlaArgTrpHisLeuThr | p. | Db 1334GGCTGCCTCGGCCCCAGCAGCAGCAGGAGGAGGAGCACATCACCT 1381 | 1280 TTAGATAATTCCTTGAAGATGTCAGGAATGGGATCTATCCTCTGACAGCCTTT | Db 1220 CCTGCAGGACCAGGAAGAAACCAGTTCAGACTTTGTACTCTCAGTCACCAGCTCTGGAA 1279 Qy 374 LeuAspLysPheLeuGluAspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAla 393 | Qy 355 ProArgProArgArgProProLeuGlnTrpArgTyrSerGluValSerPheMetGlu 373 | Oy 335 GluAsnValValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeu 354 ::: :: | Db 1100 GTGCCCTCGCTCAAACTCCTTGCGGCCCACTGCATTGTGGGACACCAACACACAC |
|---|--|---|--|--|--|--|---|--|--|--|--|--|--|--|--|---|--|---|---|
| S | D Q | D Q | Qy db | B 2 | S B 6 | ; | ag d | S B S | gg Qy | B & | οb | B 8 | g Qy | D Q | р <i>5</i> | 8 8 | S S | B & | Db |
| 394 ThrArgProLeuGlyLeuProArgValLeuAlaProProProGluGluVal 410 | 374 LeuAspLysPheLeuGluAspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAla 393 | 355 ProArgProArgArgProProLeuGlnTrpArgTyrSerGluValSerPheMetGlu 373 | 335 GluaenValValGluGluLysThrLysAlaMetAepLeuHisAlaValLeuAlaGluLeu 354 :: 1188 GAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAGTGCCGTACTGGCTGAAATC 1247 | 1128 GTGCCCTCGCTCAAACTCCTTGCGGCCCACTGCATTGTGGACACCCAACACACATGATCCCA 1187 | Higher Content of the Content of t | 2/5 ArgAlaArghisSerLeuserAsperoAsnMetArgGilDheileLeuCysCysLeuAla 294 | | 237 ValalaAspGlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet 255 | 217 IleArgAlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGlu 236 :::::: ::: | 197 ArgIlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro 216 | 177 ThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHis 196 | 157 IleLeuSerAlaLeuSerPheLeuHißAlaCyßSerProProIleIleHißGlyAßnLeu 176 | 137 LysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln 156 | 117 AlaArgValllePhelleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys 136 | | 450 CGCAAGAACTACAAGCTGCAGGAGGAAAAAGGTTCGTGCTGTGTTTGATAATCTGATTCAA 509 | 77 ArgLysAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeu 96 | 57 LeualametaspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAsp 76 | |

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Result
No.
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-Q=/cgn2_1/USPTO_spool_p/US10618941/runat_12012006_070203_14258/app_query.fasta_1.647
-Q=/cgn2_1/USPTO_spool_p/US10618941/runat_12012006_070203_14258/app_query.fasta_1.647
-DB=N_Geneseq -QFMT=fastap -SUFIX=run=-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEABS1ZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER=US10618941_9GGN_1_1_1096_grunat_12012006_070203_14258 -NCPU=6 -ICPU=3
-NO MMAR -LLARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                      Score
  2670
2612
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1: geneseqn198
2: geneseqn200
3: geneseqn200
4: geneseqn200
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                      Description
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| | ADI22646 AAS27174 ABK43562 ADB93352 | 10 4 10 | 538 910 910 | | |
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| Adi54252 cDNA enco Ado15884 4 synthes | ADI54252 ADO15884 | 12 | 1065 | 0.5 | 955 |
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| œ | ADO58748 | 12 | 1980 | . 6 | 965.5 |
| Aac64747 Secreted | AAC64747 | ب | 1606 | ٥. | • |
| Adi29383 Mouse MAR | ADI29383 | 12 | 1568 | ::: | 1106.5 |
| Human | ABZ80409 | | 2923 | ٠. | 1170 |
| Abl02019 Drosophil | ABL02019 | | 2803 | • | 1174.5 |
| | ADI29380 | 22 | 2328 | | 1360.5 |
| Aaf44682 Novel pro | AAF44682 | | 2328 | 51.0 | 1360.5 |
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| Adg10843 Human STA | ADG10843 | 10 | 2178 | | 1522.5 |
| | AAH78063 | v | 2159 | • | |
| Human | AAH14231 | 4. | 2159 | • | • |
| | ADI53948 | N | 2225 | • | • |
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| Aea61756 Human nuc | AEA61756 | | 2163 | 57.5 | |
| Adz49553 Insulin s | ADZ49553 | | 2163 | | 1534.5 |
| Adg10731 Human STA | ADG10731 | 10 | 2163 | 57. 5 | • |
| Novel F | AAF44684 | 4 | 2163 | | 1534.5 |
| Human | ABA93734 | 6 | 2158 | 57.5 | 1534.5 |
| Human | AAH14904 | 4 | 2141 | • | 1534.5 |
| Human | AAF29899 | v | 981 | 60.6 | 1617 |
| I | AAK51824 | 4 | 1501 | 82.4 | 2201 |
| | AEA61757 | 14 | 3538 | • | 2368 |
| - | ADV35041 | 13 | 3538 | • | 2368 |
| 9 Human | ADI29379 | 12 | 3304 | 90.2 | 2409 |
| Novel | AAF44681 | 4 | 3304 | • | 2409 |
| 51 CDNA 8 | 775 | 14 | 3147 | 93.6 | 249 |
| 4234 Plant | 4 | 13 | | 94.8 | |
| Adx52133 Plant ful | ADX52133 | 13 | 3846 | 96.8 | 2584 |

ALIGNMENTS

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RESULT 1
ADJ96576 standard; DNA; 3765 BP.

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ADJ96576;
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O6-MAY-2004 (first entry)
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Egen; ds; kinase; human; tyrosine protein kinase;
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Human Nim-A related protein kinase; PTK; STK; gene therapy; cancer;
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Egen; ds; kinase; human; tyrosine protein kinase;
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Egen; ds; kinase; human; tyrosine protein kinase;
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Egen; ds; kinase; human; tyrosine protein kinase;
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Egen; ds; kinase; human; tyrosine protein kinase;
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Egen; ds; kinase; human; tyrosine protein kinase;
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Egen; ds; kinase; human; tyrosine protein kinase; brain;
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CHOSTATION (STK; gene therapy; cancer; kin munomodulator; inflammatory; disorder; kin munomodulator; antiinflammatory; XX

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Homo sapiens.

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WO2004006838-A2.

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Egen; ds; kinase; NRBP2.

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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes soreening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polynucleotide sequence is a human kinase DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., c or neurological, immunological or inflammatory disorders.
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                                       GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg
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                                                                                                                     GlyPheLeuHisGluAspAspArgMetLysLeuAlaAlaPheLeuGluSerThrPheLeu
                                                                                                                                                                        ThrTyrAspLeuLeuProThrAspSerAlaGlnAspLeuAlaSerGluLeuValHisTyr
                                                                                                                                                                                                                          LysAlaArgTrpHisLeuThrLeuLeuLeuValLeuGluAspArgLeuHisArgGlnLeu
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                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a combination comprising cDNAs that are Cd differentially expressed in response to steroid treatment. Also included Cd are the following: a high throughput method for using a cDNA to detect Cd differential expression of nucleic acids in a sample; and a high Cd throughput method of screening molecules or compounds to identify a Cd ligand that specifically binds a cDNA. The sample is from a subject with Cd wilson disease and comparison of a standard defines a stage of that Cd disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combination to the molecules or compounds under combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at Cd least one molecule or compound. The molecules or compounds are regulatory corrections. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis Cd inferentially expressed in steroid-induced C3A liver cells. Note: The sequence represents a human cDNA which is differentially expressed in steroid-induced C3A liver cells. Note: The specification but was obtained in electronic format directly from USPTO or reaching the printed on the part of the printed content of the printe
                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                 Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1053; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises CDNAs that are differentially expressed in response to steroid
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 The invention describes a polynucleotide consisting
                                                          New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathoge pests, for conferring increased resistance to plant disease, or for improving yield.
                                     Claim 1;
                                                                                                                                             Liu J,
                                                                                                                                                                                          (ZHOU/)
(KOVA/)
(SCRE/)
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KOVALIC D K.

SCREEN S E.

TABASKA J E.

CAO Y.
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CC available in electronic form from the US patent office at CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide CC of the invention are also useful in physical arrays of molecules and as CC plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme CC osmotic conditions, pathogens or pests, for manipulating growth rate in CC plant cells by modification of the cell cycle pathway, for conferring CC increased resistance to plant disease, for producing galactomannan, CC lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake CC or by providing improved plant growth and development under at least one Stress condition or for modifying seed oil or protein yield and/or CC content. This sequence represents a plant full length insert
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Sequence 3837 B₽; 799 A; 1195 C; 1084 G; 759 H. 0 U; 0 Other;

Query Match: DB:

Percent Similarity: Best Local Similarity:

2.09e-250 2584.00 88.05% 88.05% 96.78%

Length: Matches: Conservative: Mismatches:

Indels: Gaps:

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Scores:

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| 158 | | 149 | δ. |
| 830 | GGGGCTGGGCGAGGATGCGGGGCGGGCTCCGCAGGCCCAGCCGCCTCTCCTGCGCCCACC | 771 | 밁 |
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| 770 | ACGGGGTTGGGGCAGCCTCGGGGACTGGGATGGTGAGGGGGTGCCCGGCGGCGCCTCGGACA 770 | 711 | 밁 |
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| 710 | | 651 | 밁 |
| 148 | AsnHisLysAlaMetAsnAlaArg | 141 | Ş |
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| 140 | PheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLysLysThrLysLys | , 121 | S |
| 590 | | 531 | 밁 |
| 120 | AsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCysAlaArgValIle | , 101 | Ş |
| 530 | | 471 | 밁 |
| 100 | AlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeuValAspHisPro | , 81 | S |
| 470 | ACGGAGGAGGGGTAGAGGTGTGGAAACGAGCTCCACTTCGGAGACAGGAAGGCCTTC | 411 | 밁 |
| 80 | | 61 | Ş |
| 410 | CGGGAGCAGGTAAAACCAAGGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATGGAC | 351 | 문 |
| 60 | | , 41 | Ş |
| 350 | | 291 | 문 |
| 40 | GluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArgTrpGlnLysArg | , 21 | S |
| 290 | | 231 | 닭 |
| 20 | MetAlaAlaProGluProAlaProArgAlaArgGluArgGluArgGluArgGluAsg | , , | Ş |
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Percent Similarity: Best Local Similarity:

2.09e-250 2584.00 88.05% 88.05%

Length:
Matches:
Conservative:
Mismatches:

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Pred. No.: Alignment

Sequence

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The invention describes a recombinant DNA construct comprising a conjunct consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at consisting of a sequence encoding an amino acid sequence conversion of the invention are also useful in physical arrays of molecules and as conjunction are also useful in physical arrays of molecules and as conjunction of the conjunction are also useful in physical arrays of molecules and as conjunction of the conjunction of the conjunction of the conjunction of the cell cycle pathway, for conferring conjunction of the cell cycle pathway, for conferring conjunction of the cell cycle pathway, for conferring conjunction of plant disease, for producing galactomannan, conjunction in plants, for improving yield by modification of conjunction of plant for improving yield by modification of conjunction or for modifying seed oil or process under at least one stress condition or for modifying seed oil or process insert content. This sequence represents a plant full length insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 26848; 15pp; English.
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(KOVA/)
(SCRE/)
(TABA/)
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) KOVALIC D K.
) SCREEN S E.
) TABASKA J E.
) CAO Y.
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  GAAATCCAGACCAATGGGGACACCCGGGTCACAGAGGAGGCCATTGCTCGCGCCAGGCAC
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                                                                                    GCTGAGCGAGAGGAACTTCGGAACCTGCACTTCTTCCCCCCAGAGTATGGAGAGGTGGCC
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                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a recombinant DNA construct comprising a CC polynucleotide consisting of a sequence encoding an amino acid sequence CC available in electronic form from the US patent office at CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide CC of the invention are also useful in physical arrays of molecules and as CC plant breeding markers. The recombinant DNA construct is useful for CC improving plant tolerance to cold, heat, drought, herbicides, extreme CC commotic conditions, pathogens or pests, for manipulating growth rate in CC plant cells by modification of the cell cycle pathway, for conferring CC increased resistance to plant disease, for producing galactomannan, CC lignin or plants, for improving yield by modification of plants, for improving yield by modification of plants or providing improved plant growth and development under at least one crombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
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            GAGGATGTCAGGAATGTACCCACTGATGAACTTTTGCAGCCACTCGACCCCTGGGG
                          GluAspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAlaThrArgProLeuGly
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                                                New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathoge pests, for conferring increased resistance to plant disease, or for improving yield.
 The invention describes a recombinant DNA construct comprising
                        Claim 1;
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(KOVA/)
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05-NOV-2001;
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CC polynucleotide consisting of a sequence encoding an amino acid sequence cavailable in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide cof the invention are also useful in physical arrays of molecules and as improving plant tolerance to cold, heat, drought, herbicides, extreme combinitions, pathogens or pests, for manipulating growth rate in cold increased resistance to plant disease, for manipulating growth rate in increased resistance to plant disease, for producing galactomannan, cold increased resistance to plant disease, for producing galactomannan, cold increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert of the invention.
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Sequence 3128 ₿P; 617 A; 973 Ç 966 ç, 572 7 0 U; 0 Other;

Best Local Similarity: Query Match: DB:

Percent Similarity: Alignment Scores: Pred. No.:

3.17e-245 2531.50 2531.50 83.47% 83.31% 94.81%

Conservative: Mismatches: Indels:

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Caenepeel S, 09-MAY-2003; 2003US-0469014P 07-MAY-2004; 2004WO-US014421 WO2005000200-A2 (SUGE-) SUGEN INC Manning ڻ و Charydczak G,

New isolated, enriched, or purified kinase nucleic acids and polypeptides, useful for diagnosing or treating, e.g. cancers, neurological and neurodegenerative diseases, cardiovascular disease, inflammatory disorders. or

2005-066508/07.

Grigoriev

ADV97865

ID NO 71; 300pp; English.

This invention relates to novel isolated, enriched or purified nucleic caid molecules that encode kinase polypeptides. Specifically, it refers to a bioinformatics strategy used to identify mammalian members of the protein and lipid kinase families. The present invention provides methods cfor identifying a substance that modulates the activity of a kinase collection of a kinase explicitly peptide, as well as a method for the detection of a kinase mucleic acid in a sample as a diagnostic tool for a disease or disorder.

CC disrupted by recombination at a nucleic acid sequence such that it croduces a phenotype, relative to the wild-type, that exhibits an absence of kinase activity. The nucleic acids and polypeptides given in the specification are useful for the diagnosis and treatment of cancer, central or peripheral nervous system diseases, psychotic and neurological disorders, neurodegenerative diseases, metabolic disorders, can be used for come a thorapy purposes and compositions. As such, they can be used for come a thorapy purposes and compositions as which they can be used for gene therapy purposes and compositions exhibit cytostatic, antimigraine, analgesic, endocrine-Gen., nootropic, tranquilizer, hypotensive, hypertensive, neuroprotective, antiparkinsonian, virucide, fungicide, antibacterial, antidiabetic, anorectic, antiarteriosclerotic, ophthalmological, antinflammatory, antiarthritic, antirheumatic, antiasthmatic, osteopathic, antiporiatic, immunosuppressive, cardiantgen, vasotropic, antiallergic and gastrointestinal-gen. This polynucleotide is a cDNA sequence that encodes a murine protein kinase c

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AAF44681 standard; CDNA; 3304

AAF44681;

27-MAR-2001 (first entry)

Novel protein kinase cDNA, SEQ ID ö 61.

RESULT 8
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AC Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antiidiabetic; antiinfertiilty; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a novel protein kinase. The nucleic acids CC and the protein kinases they encode may be used in the treatment and CC diagnosis of diseases associated with inappropriate kinase expression CC such as immune-related diseases and disorders, cardiovascular disease, complementary sequences may also be used as DNA probes in disgnostic CC complementary sequences may also be used as DNA probes in the production CC assays. The kinase expression and activity. Anti-kinase antibodies of kinase expression and activity. Anti-kinase antibodies CC antibodies of kinase expression and activity. Anti-kinase antibodies CC expression and activity. Diseases related to down regulate kinase CC expression and activity. Biseases related to kinase expression and CC activity include rheumatoid arthritis, atherosclerosis, autoimmune CC disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-cc stress related disorders, chronic inflammatory bowel disease, chronic inflammatory bowel disease, chronic plantation, rhinitis, autoimmunity, diabetes, cancers and reproductive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a compound comprising a sequence comprising 8-80 base pairs (Dp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridises with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative diseases, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated CDNA included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                                    No.:
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P-PSDB; ADI29261.
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                                                                        This invention relates to a novel screening method identified as a multi-
CC parameter high throughput screening (MPHTS) assay. Specifically, it
CC refers to an assay that utilises the disease signature of a plurality of
CC specific genes associated with a particular disease, and identifies
CC differential expression between those cells taken from individuals
CC affected by that disease and those that are not affected. The present
CC compounds to identify those that have a potential therapeutic benefit for
CC the treatment of neuropsychiatric and neurodegenerative disorders
CC this invention the said Alzheimer's disease. Accordingly, the compounds
CC well as Parkinson's and Alzheimer's disease. Accordingly, the compounds
CC of this invention exhibit various activities including neuroleptic,
CC nootropic, antinanic and antidepressant. Furthermore, the screening
CC method used in MPHTS will be automated, such that a large number of test
CC compounds may be rapidly screened with a minimal amount of labour and
CC differentially expressed in in the presence of the therapeutic compound
CC valproate, given in an exemplification of the invention.
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14-NOV-2001;
18-JAN-2002;
                                            Sequence 3538 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a compound that can treat disease or disorders, such neuropsychiatric disorder e.g., schizophrenia, or autism, comprise determining the expression of one or more efficacy genes in a cel contacted with the test compound.
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24-NOV-2003; 2003US-0524541P
                         23-NOV-2004; 2004WO-US039708
                                                                            WO2005052130-A2
                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                  Nuclear receptor binding protein 2; GTPase modulator; cancer; neoplasm; cytostatic; gene therapy; antibody therapy; drug screening; diagnosis;
                                                                                                                                                                                                                                                         Human nuclear receptor binding protein 2 (NRBP2) cDNA.
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                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                        Location/Qualifiers
                                                                                                    product= "Human nuclear receptor binding protein
                                                                                                              '*tag= a
'gene= "NRBP2"
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The present sequence is that of cDNA encoding human nuclear receptor CC binding protein 2 (NRBP2). The inventors have discovered genes that CC modify the RAC GTPase pathway in Caenorhabditis elegans and identified their human orthologs as NRBPs. The inventor provides methods for using these RAC modifier genes and polypeptides to identify NRBP-modulating CC agents that are candidate therapeutic agents that can be used in the CC treatment of disorders associated with defective or impaired RAC function or NRBP polypeptides and restore RAC function. Other preferred NRBP-cC modulating agents are nucleic acid modulatons such as antisense oligomers and RNAi that repress NRBP gene expression or product activity. NRBP-cC modulating agents may be evaluated by in vitro or in vivo assay for controls are identified as candidate RAC modulating agents. The assay system relative to controls are identified as candidate RAC modulating agents. The assay CC system may be cell-based or cell-free. NRBP modulating agents include totherapeutics), NRBP-specific antibodies, NRBP-specific antibodies, NRBP-specific antibodies, where assay for colidancers and other nucleic acid modulators, and chemical agents that colidancers and other nucleic acid modulators, and chemical agents that colidancers and other nucleic acid modulators, and chemical agents that colidancers and other nucleic acid modulators, and chemical agents that colidancers and other nucleic acid modulators, and chemical agents that colidancers and other nucleic acid modulators, and chemical agents that colidancers and other nucleic acid modulators, and chemical agents that colidancers and other nucleic acid modulators, and chemical agents that colidancers and other nucleic acid modulators, and chemical agents that colidancers and chemical agents assay as coll proteins assay, a cell colidancers and collection assay, a cell colidancers and collection assay.

A method for diagnosing a disease, especially cancer, in a patient uses a cross of the collection assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a candidate RAC pathway modulating agent using a nuclear receptor binding protein (NRBP) polypeptide or nucleic acid, useful for diagnosing or treating cancer.
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P-PSDB; AEA61759.
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Sequence 3538 BP; 806 A; 1076 C; 928 ດ 728 T; 0 U; 0 Other;

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                                                                        ProGluProPheAspSerGluThrArgLysVallleGlnMetGlnCysAsnLeuGluArg
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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                                                                    CTGAAGCTCCTGGCAGCCCACTGCTTCATCCAGCACCAGTACCTCATGCCTGAGAATGTG
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                                                                                                                                                                                                                                                                          New protein kinase polypeptides, nucleic acids and anti-kinase antibodies, useful for diagnosing and treating e.g. cancer, inflammatory, immune, cardiovascular and bone disorders.
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The present invention relates to human protein kinase. The proteins are from new human genes termed h12832, h14138, h14833, h15990, h15993, h16341 and h2252. The proteins may be used to identify modulators of their activity. The proteins may also be used to derive products for the treatment of cellular growth related disorders, malignancies, cancers, immune, inflammatory, respiratory, haematological and bone-related

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Gaps:
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RESULT 14
AAH14904
AID AAH14
AC AAH14
A
                                                                                              CC length cDNAs defined in the specification. Where a primer set complises:

CC (a) an oligo-dT primer and an oligonucleotide which comprises one of the 5602 complementary strand of a polynucleotide which comprises one of the 5602 cc complementary strand of a polynucleotide comprises one of the 5602 cc oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end cc complementary to a sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the compount of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in cc gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers era also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC CNASS easily without any specialised methods. AAH03166 to AAH13628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without any specialised methods. AAH03166 to AAH03628 and CC CNASS easily without easily without easily easily easily easily easily easily easily e
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
disgnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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Sugiyama T,
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2000JP-00183767.
2000JP-00241899.
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K, Otsuki
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Best Local Similarity:
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GluAsnValValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeu 354
                      GTGCCCTCGCTCAAACTCCTTGCGGCCCACTGCATTGTGGGGACACCAACACGATGATCCCA 1137
                                                                                                                                                                          AlaValLeuGluIleGlnThrAsnGlyAspThrArg---ValThrGluGluAlaIleAla 274
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                                                                   TCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTTCCACCCAGCATTGTTTGAA
                                                                                     ArgAspProAlaArgArgProSerAlaHisSerLeuLeuPheHisArgValLeuPheGlu 314
                                                                                                                                                            GCAGTGCTGGAGATTCAGGGCAATGGAGAGTCCTCATATGTGCCACAGGAAGCCATCAGC
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                                                                                                                    Human cDNA sequences and clones derived from human fetal brain, kidney, melanoma, testis and amygdala cDNA libraries, useful in screening and therapy.
                                                                                                                                                                                                                            WPI; 2002-055860/07.
P-PSDB; ABB05696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA93734;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain derived cDNA clone fbr2_78d18.
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The present invention describes assemblages and computer readable media comprising novel human cDNA sequences and clones derived from human

Claim 1;

Page 215-216; 611pp; English

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                 AlaValLeuGluIleGlnThrAsnGlyAspThrArg---ValThrGluGluAlaIleAla
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Command line parameters:

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-Op-Cgn2 1/USFTO_spool p/US10618941/runat 12012006 070204_14281/app_query.fasta_1.647
-DB=EST -OPMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blts -STRAT=1 -END=-1 -MATRIX=blosum62 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10618941 @CRN 1 1 8010 @runat 12012006 070204 14281 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
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AK046142 Mus muscu
AY408905 Mus muscu
AL834530 Homo sapi
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| | • | | • | • | • | • | • | • | • | | • | • | • | • | | • | | | • | • | | • | • | | 43.5 | | • | • | • | • | • | • | | | | | |
| 819 | 586 | 950 | 730 | 756 | 1122 | 922 | 637 | 1001 | 929 | 869 | 897 | 898 | 1382 | 643 | 959 | 911 | 996 | 651 | 725 | 770 | 899 | 1028 | 700 | 716 | 841 | 673 | . 859 | 2923 | 729 | 825 | 927 | 899 | 2181 | 2086 | 2181 | 2158 | 2137 |
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| 9075 | 3547 | BQ648254 | 3260 | 4 | BI410402 | CR982195 | CN790575 | BQ716004 | CX917126 | CX566377 | BU839694 | BQ649309 | DN656596 | CN358567 | BQ652622 | BU508281 | BI650160 | CB557694 | BG913260 | CN218030 | BF299723 | AL532940 | CN358568 | CV105566 | CO248961 . | DN998004 | CK476491 | AF318376 | CD354461 | BI645887 | 8 | 8 | AK077440 | 1 | 58669 | HSM801650 | CR604477 |
| | | AGENCOUR | CB326067 UI-R-DZ0- | BF134441 60178483 | BI410402 60296491 | CR982195 CR982195 | CN790575 4125180 | BQ716004 AGENCOUR | CX917126 JGI CAAN5 | CX566377 UI-M-IB0 | BU839694 AGENCOURT | BQ649309 AGENCOUR | DN656596 CEC24-A06 | CN358567 17000532 | BQ652622 AGENCOURT | BU508281 AGENCOUR | BI650160 60329625 | CB557694 AMGNNUC: | BG913260 60281194 | CN218030 RJA022G0 | BF299723 60202922 | AL532940 AL532940 | CN358568 17000531 | CV105566 AGENCOURT | CO248961 AGENCOUR | DN998004 TC107239 | CK476491 AGENCOUR | AF318376 Homo sap | UI-M-GMO | 4588 | 10189 | 98804 CR | 77440 Mu | 1118 fu | 8669 Pongo py | 136682 Homo | CR604477 full-len |
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DNA Sequencing by: University of Idwa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and
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This clone has the following problem: clone
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Submitted (25-MAR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                ThrGluGluGlyValGluValTrpAsnGluLeuHisPheGlyAspArgLysAlaPhe
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/tissue_type="Brain, mouse
/clone_lib="NIH_BMAP_EW0"
/lab_host="DH10B"
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 CTATCCACTGATGAACTTTGCGGCTGCTCGGCCCTTGGGGCCTTCCCCGTGTGTTGGCCCC
                  eTyrProLeuMetAsnPheAlaAlaThrArgProLeuGlyLeuProArgValLeuAlaPr
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El (Dases 1 to 3729)

RS Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S.,

Carninci, P., Frange, C., Raha, S.S., Loquellano, M.A., Peters, G.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
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                                                               Submitted (04-SEP-2002) National Institutes of Health, Gene Collection (MGC), Betheada, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria;
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                                                                                                                                     Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
A.N., Gibbs, R.A.
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DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
  oProIleIleHisGlyAsnLeuThrSerAspThrIlePheIleGlnHisAsnGlyLeuIl
                                               CTGGAAGCGCTGGTGCACGCAGATCCTGTCTGCGCTCAGCTTCCTGCACGCCTGCAGCCC
                                                                          aTrpLysArgTrpCysThrGlnIleLeuSerAlaLeuSerPheLeuHisAlaCysSerPr
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                                                                                                                                CAAGCAATTCCTCAAAAAGACCAAGAAGAACCACAAGGCCATGAACGCCCGGGTATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCCTGAGCTCGCACCGTGCAGGTCATCTTCATCACAGAGTACGTGTCATCAGGCAGCCT
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                                                                                                                                                                                                                                                                                                          AGCGGGCTGGGGCAGCCACGGGGACAGGACGGGGTTGGGGCAGCCTCGGGGACTGGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/clone="IMAGE:5180619"
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2037.50
75.59%
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Matches:
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| ralaGlnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGlu | 389 tASRPheAlaAlaThrArgProLeuGlyLeuProArgValLeuAlaProProProGluG1 409 | 945 CCCCGGGGCTCTTCCAGGACAAATTTCCTGGAGGAGCTCAGGAATCTACCACTGAT 1184 | | |
|---|---|--|---|--|
| KOya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitch,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. TITLE Direct Submission JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 17-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, | FANTOM Consortium. TITLE Functional annotation of a full-length mouse cDNA collection JOURNAL Nature 409, 685-690 (2001) REFERENCE 5 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs JOURNAL Nature 420, 563-573 (2002) REFERENCE 6 (bases 1 to 2163) RAUTHORS Adachi,J., Alzawa,K., Akimura,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiracka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., | 3 Shi Shi Kon Kon Yama Yama Yama Gen RIX Beg | REFERENCE 1 AUTHORS Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning JOURNAL Meth. Enzymol. 303, 19-44 (1999) PUBMED 2 REFERENCE 2 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes JOURNAL Genome Res. 10 (10), 1617-1630 (2000) PUBMED 11042159 | RESULT 3 AKO46142 LOCUS AKO46142 ACCESSION AKO46142 ACCESSION AKO46142 ACCESSION AKO46142 AKO46143 AKO46142 AKO46143 AKO |

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                 97
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Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                             GluArgGluAspGluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArg
ValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCys
                                            LeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAsp
                                                                                                                                                                TGGCAGAAGAGGCGAGAAGAGGTGAATCAGCGTAATGTACCAGGCATTGACAGTGCATAC
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/kvlmqcniseysegvgehltillkledklnelscolmpnesifplaaelgolgfis
/saagslssvleetlnkfnfsrnstlntatvtvsvvelf"
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2163
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/clone_lib="RIKEN full-length enriched mouse
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:B230344L17"
/db_xref="taxon:10090"
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               LeuLeuLeuValLeuGluAspArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThr
                                                                             ValIleGlnMetGlnCysAsnLeuGluArgSerGluAspLysAlaArgTrpHisLeuThr
                                                                                                                                                                                                   ThrArgProLeuGlyLeuProArgValLeuAlaProProProGluGluVal-------
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Mus musculus (homus musculus
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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                              LeuAlaMetAspThrGluGluGlyValGluValTrpAsnGluLeuHisPheGlyAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence was made by sequencing based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                  /gene="NRBP"
/locus_tag="HCM3379"
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                           -----GlnLysAlaLysThrProThrProGluProPheAspSerGluThrArgLys
ValIleGlnMetGlnCysAsnLeuGluArgSerGluAspLysAlaArgTrpHisLeuThr
                                                                                                                                                              LeuAspLysPheLeuGluAspValArgAsnGlyIleTyrProLeuMetAsnPheAlaAla 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp43412411) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
Please contact RZPD for ordering:
Please contact RZPD for ordering:
Purther information about the clone and the sequencing project in available at http://mips.gsf.de/projects/cdna/.

Location/Qualifiers
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heldelberg.de;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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QCULERSEDKARMHLTILLVULEDRLHRQLTYDLLFTDSAQDLASELVHYGFLHEDDRM
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/db_xref="mRNA"
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/clone_Tib="434 (synonym: htes3
DH10B; sites NotI + SalI"
/dev_stage="adult"
/note="hypothetical protein (Ra
N-terminus truncated"
                                                                                                                                                                                                                                      /gene="DKFZp434I2411"
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240 293 180 273 120 253 60

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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Pan troglodytes NRBP gene, VIRTUAL
genomic survey sequence
AY408904
AY408904.1 GI:39764872
GSS.
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Direct Submission
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This sequence was made by sequencing genothem based on alignment.
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Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                  LeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAsp
                                           TTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAAG
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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GTGAAGACTTGTCGAGAAGAGCAGAAGAATCTACACTTCTTTGCACCAGAGTATGGAGAA
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                  AspSerAlaGInAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAsp
                                                      VallieGlnMetGlnCysAsnLeuGluArgSerGluAsgLysAlaArgTrpHisLeuThr
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1 (bases 1 to 1608)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
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Science 302 (5652), 1960-1963
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                        LeuAlaMetAspThrGluGlyGlyValGluValValTrpAsnGluLeuHisPheGlyAsp
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.

1 (bases 1 to 2137)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished
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CR604477.1 GI:50485284
HTC; CNSLT_CDNA.
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2 (bases 1 to 2137)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                      LeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAsp
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="CSODIO08YI22"
/tissue_type="Placenta_Cot
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                    GTCGTGCCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAAG
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                                                                                                                                        ThrArgProLeuGlyLeuProArgValLeuAlaProProProGluGluVal------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp564D1878) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomicorschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp564D1878
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
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AL136682.1
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1 (bases 1 to 2158)
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Mewes,H.W., Weil,B., Amid,C.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
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/db_xref="Unifred/Trembl;Q9UHY1"
/trembl;C9UHY1"
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                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="brain"
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X1-2blue; sites NotI + SalI"
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/db_xref="RZPD:DKFZp564D
                                                                                                                                                                                                                                                    /gene="DKFZp564D1878"
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_xref="taxon:9606"
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Osanger,A., Fobo,G., Han,M. and
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NGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLK LLAAHCIVGHQHHIPENALEBITKNHDTSAVLABIPAGPGREPYQTLYSQSPALELDK FLEDVENGIYPLTAFGLPRPQQPGEVTSPVVPPSVKTPTPBPAEVETRKVVLMQCN IESVEBGVKHLITLLLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEADQSRLT SLLEETLNKFNFARNSTLNSAAVTVSS"

Percent Similarity: Best Local Similarity: ArgAlaArgHisSerLeuSerAspProAsnMetArgGluPheIleLeuCysCysLeuAla AlaValLeuGluIleGlnThrAsnGlyAspThrArg---ValThrGluGluAlaIleAla GTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTT ValAlaAsp---GlyThrAlaValAspIlePheSerPheGlyMetCysAlaLeuGluMet GTGAAGACTTGTCGAGAAGAGCAGAAGAATCTACACTTCTTTGCACCAGAGTATGGAGAA IleArgAlaGluArgGluGluLeuArgAsnLeuHisPhePheProProGluTyrGlyGlu ThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHis IleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeu LysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln AlaArgValllePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys TTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGGCTGACATTAAAGAGAACAAG ValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCys ArgLysAlaPheAlaAlaHisGluGluLysIleGlnThrValPheGluGlnLeuValLeu TGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGAA LeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAsp TGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATAC GAGGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTTGGAAGAGTCGCCCTGTGGGCGC GluArgGluAspGluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArg 36 ArgIlePheSerAsnAlaLeuArgProProThrAlaLeuProAspAspLeuArgSerPro ACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAGATTGGCTCTGTG-----AAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACAA GCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAAG CGCAAGAACTACAAGCTGCAGGAGGAAAAGGTTCGTGCTGTGTTTGATAATCTGATTCAA TrpGlnLysArgArgGluGlnValAsnGlnGlyAsnMetProGlyLeuGlnSerThrPhe (1-507) x HSM801650 TGGAGATTCAGGGCAATGGAGAGTCCTCATATGTGCCACAGGAAGCCATCAGC 7.15e-152 1534.50 73.54% 61.62% 57.47% (1-2158)Length: Matches: Conservative: Mismatches: Indels: Gaps: = -----GCTCCTGACACTATCAACAATCAT recatetetecactegagate 2158 305 59 102 29

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sequencing consortium of the German Genome Project. This clone (DKFZp459G2032) is available at the RZPD Deutsches (BKFZp459G2032) is available at the RZPD Deutsches (BKFZp459G2032) is available at the RZPD Deutschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp459G2032 Further information about the clone and the sequencing project is
                                                                                                           Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
                                                                                                                                                                                                                                                                                                                                      Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pongo pygmaeus mRNA; cDi
CR858669
CR858669.1 GI:55728271
                                                                                                                                                                                                                                     Koehrer, K., Beyer, A., Mewes, H. Pobo, G., Han, M. and Wiemann, S. The German CDNA COnsortium Direct Submission
                                                                                                                                                                                                                     Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1,
                                                                                                                                                                                                                                                                                                                                                                                                                    Pongo pygmaeus (orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluAsnValGluGluLysThrLysAlaMetAspLeuHisAlaValLeuAlaGluLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuLeuLeuValLeuGluAspArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThr
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В.,
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Percent Similarity:
Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluArgGluAspGluSerGluAspGluSerAspIleLeuGluGluSerProCysGlyArg
                                                                                                                                                                                                                                                                                                                     ValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCys
                                                                                                                                                                                GCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAAG
                                                                                                                                                                                                          AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLys
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IleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLeu
                                                                          AAGACCAAAAAGAACCACAAGACCATGAATGAAAAGGCATGGAAGCGTTGGTGCACAA
                                                                                                        LysThrLysLysAsnH1sLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGln
                                                                                                                                                                                                                                                                                     TTGGAGCATCTTAACATTGTTAAGTTTCACAAATACTGGGCTGACATTAAAGAGAACAAG
                                                                                                                                                                                                                                                                                                                                                                                        CGCAAGAACTACAAGCTGCAGGAGGAAAAAGGTTCGTGCTGTGTTTGATAATCTGATTCAG
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GSVAPDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQG
NGSSSYVPOBAISSAIQLEDDFLOREFIOKCLQSEPAREPTARELLFHPALFEVPSLK
LLAAHCIVGHQHMIPENALESITKNWDTSAVLAEIDAGPGREPVQTLYSQSPALELDK
FLEDVRNGIYELTAFGLPFDQPQQGESVTSPVVPPSVKTTTPEBABVETRKVVLMQCN
ISSVEEGVKGHLTILLKKLEDKLNRHLSCDLMPNENIFBLAAELVQLGFISEADQSRLT
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DH10B; sites SfilA + SfilB"
/dev_stage="adult"
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/mol_type="mRNA"
/db_xref="taxon:9600"
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full-length
                                                                                                                   ArgMetLysLeuAlaAlaPheLeuGluSerThrPheLeuLysTyr
                                                                                                                                                                                        AspSerAlaGlnAspLeuAlaSerGluLeuValHisTyrGlyPheLeuHisGluAspAsp
                                                                                                                                                                                                                                                          LeuLeuLeuValLeuGluAspArgLeuHisArgGlnLeuThrTyrAspLeuLeuProThr
                                                                                                                                                                                                                                                                                                                        VallleGlnMetGlnCysAsnLeuGluArgSerGluAspLysAlaArgTrpHisLeuThr
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                                                                                                                                                               GAGAATATCCCTGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGAC
                                                                                                                                                                                                                                                                                                        GTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGAGGAGTCAAACACCACCTGACG
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Submitted (20-JUL-2004) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail:
- Web: www_genoscope.cns.fr)
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HTC; CNSLT_CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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mol type="mRNA"

/db_xref="taxon:9606"

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                                         ArgMetLysLeuAlaAlaPheLeuGluSerThrPheLeuLysTyr 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hara, A., Hashizume, W., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Ohazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Takaku, Akahira, S., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                           Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2181)
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AK077440.1 GI:26097350
HTC; CAP trapper.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FANTOM Consortium.
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AK077440

2181 bp mRNA linear HTC 03-APR-2004
Mus musculus 8 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:5730409G13 product:SIMILAR TO NUCLEAR
RECEPTOR BINDING PROTEIN (HLS7-INTERACTING PROTEIN KINASE) homolog

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Euteleostomi;

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) ដ genes

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

Phase CDNA H collecti Team and

Exploration functional Research annotation

Carninci, P.

Ohsato, N.,

Yokohama

FEATURES

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US-10-618-941-99 (1-507) x AK077440 (1-2181)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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                                                                                                                                                                              9AlaArgValIlePheIleThrGluTyrValSerSerGlySerLeuLysGlnPheLeuLy
                                                                                                                                                                                                                                      uValAspHisProAsnIleValLysLeuHisLysTyrTrpLeuAspThrSerGluAlaCy 116
                                                                                                                                                                                                                                                                                                                                                              eLeuAlaMetAspThrGluGluGlyValGluValValTrpAsnGluLeuHisPheGlyAs 76
uThrSerAspThrIlePheIleGlnHisAsnGlyLeuIleLysIleGlySerValTrpHi
                           GATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCTCCCATCATCCATGGGAACCT
                                                  nIleLeuSerAlaLeuSerPheLeuHisAlaCysSerProProIleIleHisGlyAsnLe
                                                                                                                  sLysThrLysLysAsnHisLysAlaMetAsnAlaArgAlaTrpLysArgTrpCysThrGl
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2162. .21
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140. .1749
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/clone="5730409G13"
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/strain="C57BL/6J"
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/clone_lib="RIKEN full-length enriched mouse
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EST.
Homo sapiens (human)
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Unpublished (2005)
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http://www.rzpd.de/cgi- bin/products/cl.cgi?CloneID=RZPDp9017B1314
contact RZPD (product- support@rzpd.de) for further information.
Primer name: qe3_4, Primer sequence: CGGATAACAATTCACACAG.
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Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9017 Contact:
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/tissue_type="T-Lymphocytes"
/dev_stage="adult"
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/db_xref="taxon:9606"
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/clone_lib="RZPD no.9017"
/note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Ligenoscope - Cens.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Livitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAGO70ZB10_CS06698_2.
                                                                                                                                                                                                     Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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               AsnLeuGluArgSerGluAspLysAlaArgTrpHisLeuThrLeuLeuLeuValLeuGlu
                                                                          LysThrProThrProGluProPheAspSerGluThrArgLysVallleGlnMetGlnCys
                                                                                                                                            ThrArgProLeuGlyLeuProArgValLeuAlaProProProGluGluValGlnLysAla
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODN002YIO9"
/tissue_type="ADULT BRAIN"
/dev_stäge="adult"
/dev_stäge="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT_6
vector. Library was not normalized."
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM.1800 row: n column: 13
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 825)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectio
Unpublished (1999)
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                                                                                 (1-507)
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab host="DH10B"
/lab host="DH10B"
/clone_lib="NCI_CGAP_Mam3"
/clone_stage="10 months"

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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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Search completed: January 14, 2006, 00:46:08 Job time: 4643 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: /ggn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-862-027-10
US-09-933-750C-20
US-09-934-613-20
US-09-934-613-20
US-09-945-473E-36
US-09-862-027-36
US-09-345-473E-34
US-09-862-027-34
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US-09-862-027-767-3173
US-09-862-027-767-3173
US-09-864-866-60
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US-10-010-720-28
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Sequence 10, Appl
Sequence 20, Appl
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Sequence 7299, Ap
Sequence 10, Appl
Sequence 36, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 40, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 28, Appl
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Sequence 54, Appl
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| | 241 T 246 T | 181 I 192 I | 121 F 132 F | 61 T 72 T | 12 3 | atch cal 30 | SULT 1 -09-345-473E-10 SEQUENCE 10, App PALENT NO 65589 GENERAL INFORMAT APPLICANT: HOOG TITLE OF INVENT FILE REFERENCE: CURRENT APPLICA CURRENT FILING NUMBER OF SEQ I SOFTWARE: FASTS SOFTWARE: FASTS SEQ ID NO 10 LENGTH: 326 TYPE: PRT ORGANISM: Homo FEATURE: NAME/KEY: VARI LOCATION: (1). OTHER INFORMAT | | 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 |
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| | FGMCALEMAVLE | FIQHNGLIKIGSVWHRIFSN | SSLKQFLK SSLKQFLK | WNEIHFGI | RRAREREF RRAREREF | 59.2 y 97.4 rvative | tion artin NO. 00/18 NUMB: 19 S: 62 or Wi iens | | 954 954 954 954 982 982 1911 1911 1939 1939 1939 1939 1999 20004 20004 86 |
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| | IQTNGDTRVTE | ALRPPTALPD ALPD | YVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALS | BEGVEVVMNELHFGDRKAFAAHEEKIQTVFEQLVLVDHI | MAAPEPAPRAREREREREDESEDESDILEESPCGRWQKDREQVNQGNMPGLQSTFLAMD | Score 1580; DB 2; Pred. No. 1.2e-145; 0; Mismatches 2; | US/09345473E 6558903el Kinases and Uses 13781 13781 199-06-30 199-06-30 19dows Version 4.0 | ALIGNMENTS | US-10-010-720-38 US-09-854-856-22 US-10-010-720-22 US-10-010-720-64 US-10-010-720-64 US-09-854-856-64 US-09-854-856-68 US-10-010-720-68 US-10-010-720-16 US-10-010-720-16 US-10-010-720-16 US-10-010-720-16 US-10-010-720-16 US-10-010-720-16 US-10-010-720-58 US-09-854-856-58 US-09-854-856-62 US-09-854-856-62 |
| | BAIARARHSLSDPNMRBFILCCLARDPARR 300 | DLRSPIRAEREELRNLHFFPPEYGEVADG 240 | ALSFLHACSPPIIHGNLTSDT 180 | FEQLVLVDHPNIVKLHKYWLDTSEACARVI 120 | SPCGRWQKRREQVNQGNMPGLQSTFLAMD 60 | Length 326; Indels 6; Gaps 1; | Thereof | | Sequence 22, Appl Sequence 22, Appl Sequence 6, Appli Sequence 6, Appli Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 18, Appl Sequence 32, Appl Sequence 32, Appl Sequence 16, Appl Sequence 58, Appl Sequence 58, Appl Sequence 58, Appl Sequence 62, Appl Sequence 62, Appl |

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APPLICANT: Hodge, Martin R.

FILE REFERENCE: 35800/234862

CURRENT APPLICATION NUMBER: US/09/862,027

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: US 09/345,473

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 82

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10
                                        GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVESTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESSEDENCE ADDRESS:
                                                                                                                                                                                                                                                                    RESULT 3
US-08-933-750C-20
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Best Local S
Matches 301
                                                                                                                                                                                                                                     Sequence 20, Application US/08933750C Patent No. 5932442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Applica Patent No. 6858418 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(326)
OTHER INFORMATION: Xaa = Any Amino Acid
-09-862-027-10
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TYPE: PRT
ORGANISM: Homo sapiens
                              ADDRESSEE:
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                E: Incyte Pharmaceuticals,
3174 Porter Drive
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Pred. No. 1.2e-145;
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; CLONE: 864683
US-08-933-750C-20
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Best Local Similarity 61.6%;
Matches 305; Conservative 5
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LENGTH: 535 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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COUNTRY: US
ZIP: 94304
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                                                                                                                                                                                    RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM
                                                                                                                                                                                                                                                                                                                                                                                                KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                          RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD
 OSRLTSLLEETLNKF
                              RMKLAAFLESTFLKY 502
                                                             VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAAELVQLGFISEAD
                                                                                                                                                LDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEV-----QKAKTPTPEPFDSETRK
                                                                                                                                                                                                                                                AVLEIQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFE
                                                                                                                                                                                                                                                                               AVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE
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                                                                                                                          LDKFLEDVRNGIYPLTAF-----GLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRK
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518
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Pred. No. 7e-141;
9; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102;
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29;

Gaps

76

163

221

427

314 269 255

329

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APPLICATE:
FILING DATE:
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0356 U
TELECOMMUNICATION INFORMATION:
TRUEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/09234613
PATENT NO. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Sahh, Purvi
APPLICANT: Sahh, Purvi
APPLICANT: AN-Young, Janice
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US-09-234-613-20
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Best Local S
Matches 305
                                                                                                                                                                                                                                                                                                                                            -09-234-613-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUTO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                         CLONE: 864683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                          164
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                                                                                                                         104 RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK
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                                                                                                                                                                                                                                                                  h 57.5%; Score 1534.5; DB 2; Similarity 61.6%; Pred. No. 7e-141; 05; Conservative 59; Mismatches 102;
RIFSNALRPFTALPDDLRSPIRAEREELRNLHFFPPBYGEVAD-GTAVDIFSFGMCALEM
                                                       KTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV--
                                                                              KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196
                                                                                                                                                            RKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Incyte Pharmaceuticals, 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                             BRAITUT03
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                                                                                                                                                                                                                                                                    Indels 29;
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                      255
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FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FABSEQ for Windows Version 4.0

SEQ ID NO 7299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 562
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7299
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                        191
                                                                                                                                                              197
                                                                                                                                                                                                                         137 KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWH 196
                                                                                                                                                                                                                                                                                 131 RKNYKLQEEKVRAVFDNLIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLK
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                                                                                                                                                                                                                                                                                                                                                               71 EEBESEDESEILEESPCGRWQKKREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSE 130
                                                                                                                                                                                                                                                                                                                                                                                    17 EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGD
                                                                                                                                                          RIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVAD-GTAVDIFSFGMCALEM
VHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPR-PRRPPLQWRYSEVSFME
                                       AVLEIQGNGESSYVPQEAISSAIQLLEDPLQREFIQKCLQSEPARRPTARELLFHPALFE
                                                                               AVLEIQTNGDTR-VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFE
                                                                                                                     -----APDTINNHVXTCREEQXNLHFFAPEYGEVTNVTTAVDIYSFGMCALEM
                                                                                                                                                                                                  KTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1534.5; DB 2;
Pred. No. 7.5e-141;
9; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                              102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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373
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                                                         Best Loc
Matches
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                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PO5101/97

FILING DATE: 13-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP0422/97

FILING DATE: 18-NOV-1997

PRIOR APPLICATION NUMBER: International PCT Application APPLICATION NUMBER: 1998

ATTORNEY/AGENT INFORMATION:

NAME: DIGIGLIO, FRANK S

REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                        TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: (US only) ANTALIS Toni Marie and HOODER John TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS: ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: USA
                                                                                                                       TOPOLOGY: 1:
                                                                                                                                                                                                              REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/023,942A FILING DATE: 13-FEB-1998 CLASSIFICATION: 435
                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374
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                                                          301;
        44
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                                                                     Similarity
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     EEEEESEDESEILEESPCGRWQKRREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSE
                   EREDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNBLHFGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDLMPNENIPELAABLVQLGFISEAD
                                                          Conservative
                                                                                                                                      linear
                                                                                                                         protein
                                                       56.5%; Score 1508.5;
60.8%; Pred. No. 2.4e
:ive 60; Mismatches
                                                                                                                                                                                                                                                       11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version
                                                       .5; DB 2;
2.4e-138;
hes 105;
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25
                                                         Indels
                                                                                 Length
                                                                                 535,
                                                         29;
                                                       Gaps
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RESULT 8
US-09-862-027-36
US-09-862-027-36
Sequence 36, Application US/09862027
Patent No. 6858418
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US-09-345-473E-36
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GENERAL INFORMATION:
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 231
TYPE: PRT
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CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
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TITLE OF INVENTION: No. 6558
FILE REFERENCE: 35800/183781
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: C. elegans
                                                                                                                    79 AFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKT 138
                                                                                                                                                                                                               23 DSDADGAEEILEESPDKRWSKRREQVKQRDVPGIDVAYLAMDNETGNEVVWNEVQFSERK
                                                                                                                                                                                                                                                                                                    Similarity
RKAGSSLSIKAWKKWTTQILSALNYLHSSDPPIIHGNLTCNTVFIQQNGLIKIG 196
                                  KKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIG 192
                                                                                       NFRAQEEKINAVFDNLTQLVHTNLVKFHKYWTDSKSEKPRIIFITEYMSSGSMSAFLQRT
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                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                           20.3%; Score 543; DB 2;
56.3%; Pred. No. 1.2e-44;
tive 31; Mismatches 45
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GENERAL INFORMATION:

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; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: NO. 6658418el Kinases and Use;
FILE REFERENCE: 35800/234652;
; CURRENT APPLICATION NUMBER: US/09/862,027;
; CURRENT FILING DATE: 2001-05-21;
PRIOR APPLICATION NUMBER: US 09/345,473;
; PRIOR FILING DATE: 1999-06-30;
; NUMBER OF SEQ ID NOS: 82;
; SOFTWARE: FASTSEQ for Windows Version 4.0;
; SEQ ID NO 36;
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; ORGANISM: C. (
US-09-345-473E-35
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US-09-345-473E-35
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TITLE OF INVENTION: NO. 6558903el Kinases a
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Applica Patent No. 6558903 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   Matches 116;
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Best Local (
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TYPE: PRT
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Similarity 56.3%;
                                                                                                   RNGIYPLMNFA-----LG
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      LPGQSSQPSGTTTNTNGPSSIGKSASPEAVDKKIGEVTSTESTSKVEVEVNGANVTIGSS
                                        LPRVLAPP----
                                                                     RNGIYPLTAFAPLAHQPSTTLRAYSNTNPSTLITTDISAPSSTHPSANSTITAETSVNTS
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GENERAL INFORMATION:
APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558903el Kinases and
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
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RESULT 11
US-09-345-473E-34
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US-09-862-027-35
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CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
Sequence 34, Application US/09345473E Patent No. 6558903
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APPLICANT: Hodge, Martin R.
APPLICANT: TAVENTION: No. 6858418el Kinases
FILE REFERENCE: 35800/234862
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Best Local Similarity
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ORGANISM: C.
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                                                                                                                                                                                                                                                                                                                                                                                                       382 RNGIYPLMNFA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                           134 HAIVDSKKY--EDVSESAFRIKD-NETIAATSKLR----EMAYCQVAAFQVDLEKFLDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 HCFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRPPLQWRYSEVSF--MELDKFLEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 TR--VTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 PDDLRSPIRAEREELRNLHFFFPEYGEVADGT-AVDIFSFGMCALEMAV---LEIQTNGD
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                                                                                                                                                                                                                                                                                                                    LPRVLAPP----
                                                                                                                    LTTSINKGDNPETLTENLITHGFMCQLD 388
                                                                                                                                                                                                 NGRDAGSPTPEEEGEPNGERDMRLENRHILEINVHIENEE-----MSIVILLEDQMHRQ 360
                                                                                                                                                                                                                                       ----AKTPTPE-----PFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQ 459
                                                                                                                                                          LTYDLLPTDSAQDLASELVHYGFLHEDD 487
                                                                                                                                                                                                                                                                                LPGQSSQPSGTTTNTNGPSSIGKSASPEAVDKKIGEVTSTESTSKVEVEVNGANVTIGSS
                                                                                                                                                                                                                                                                                                                                                              RNGIYPLTAFAPLAHQPSTTLRAYSNTNPSTLITTDISAPSSTHPSANSTITAETSVNTS
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Pred. No. 8.9e-32;
7; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                   PEEVQK---
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Uses

272 304 213 251

424 309

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Sequence 34, Application US/09862027
Patent NO. 6858418
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
ITILE OF INVENTION: NO. 6858418el Kinases and FILE REFERENCE: 35800/234862
CURRENT APPLICATION UNMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR TILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 516
TYPE: PRI
OBSANITM: Apphilocols thalian.
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US-09-862-027-34
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US-09-862-027-34
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 34
LENGTH: 516
                                                                                                  Matches
                                                                                                                      Query Match
Best Local
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Best Local Similarity
Matches 119; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
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                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALEMAVLEIQTNGDT-----RVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAH 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHN-GLIKIG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCSSEDLDRLYSEVHLLKTLKHKSIIKFYTSWIDHQH--MTINLITEVFTSGNLRQYRKK
                      RODENNSEEEFVEIDPTGRYGRYKEVLGKG---AFKEVYRAFDQLEGIEVAWNQVKLDDK
                                                            REDESEDESDILEESPCGRWQKRREQVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSVAIEMVEELDLTDDQD--ISTIAKMIDTEIHSHIP-DWTPSRLIGDDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPT----DSA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SEVGLITVEGORKDL-NTIFLKLRITDSK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HKCVDLRALKKWSRQILEGLVYLHSHDPPVIHRDLKCDNIFINGNQGEVKIGDLGL
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                                                                                                  13.9%;
llarity 25.3%;
Conservative 88
                                                                                                                                                                                                  thaliana
                                                                                                    88;
                                                                                              Score 372; DB 2; Length 516;
Pred. No. 1.9e-27;
8; Mismatches 176; Indels
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US-09-345-473E-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/09345473E
Patent NO. 6558903
GENERAL INFORMATION:
APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558903el Kinases and FILE REFERENCE: 35800/1813781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 199-06-30
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PastSEQ for Windows Version SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.8%;
Best Local Similarity 25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305
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                                                                                                                                                                                                                                                                                                                                                                                                            10 RAREREREDES-----EDESDI----LEESPCGRWQKRREQVNQGNMPGLQSTFL 57
LCCLARDPARRPSAHSLLFH--RVLFEVHS-LKLLAAHCFIOHQYLMPENV----VEEKT 342
                                                                                                                                                                                                                                                                                              GLDTETGVAVAWCELQ--ESKLNKTERQRFREEAEMLKDLQHPNIVRFYDYW-ESADLCG
                                                                                                                                                                                                                  KRKYIVLVTELMTSGTLKMYLKRFKRINIKVV----LKSWCRQILKGLSFLHTRNPPVIH
                                                                                                                                                                                                                                          AMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACA 117
                                                                                                                                                                                                                                                                                                                                                                      RARKEQEKREEEEKAARRIDVEDDFDAQEKPIDKSKNGRFLKFDEELGRGS---FKTVFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALEMAVLEIQTNGDT-----RVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAH
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                                                            EMYEEMYDESVDVYAFGMCLLEMVTGEYPYSECMNPATIYRKVISGVKPE-------
                                                                                              EYGEVADGTAVDIFSFGMCALEMAVLEI----QTNGDTRVTEEAIARARHSLSDPNMREFI
                                                                                                                                        RDLKCDNIFITGTTGSVKIGDLGLATLKNK-----SFAKSVIGTPEFMAP
                                                                                                                                                                          GNLTSDTIFIO-HNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPT----DSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 368.5; DB 2;
; Pred. No. 2.2e-26;
88; Mismatches 188;
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289

268

223

173

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Sequence 40, Application US/09862027

PATCHI NO. 6858418

GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
ITILE OF INVENTION: No. 6658418e1 Kinases and Us.
FILLE REFERENCE: 35800/234662

CURRENT APPLICATION NUMBER: US/09/862,027

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: US 09/345,473

PRIOR APPLICATION NUMBER: US 09/345,473

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 82
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US-09-862-027-40
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Best Local Similarity
Matches 128; Conserv
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SEQ ID NO 40
LENGTH: 1601
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461 TYDLLPTDSAQDLASELVHYGFLHEDDRMKLAA 493
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                                                     ----DSPDEVVQQMIEQQHIPDEDTRMITKL----IKDKV--
                                                                                     RVLAPPPEEVQKAKTPTPEPFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQL
                                                                                                                                                                                             --CFSRIPAQYPEIREIIDRCIRVRREERSTVKQL----LVDDFFTPEDLIGIRVEIKN
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25.0%;
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Pred. No. 2.2e-26;
8; Mismatches 188;
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Search completed: January 12, Job time: 26 secs
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US-09-270-767-31733
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                                                                                                                                                                                                                                                                                                                    APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31733
                                                                                                                                                                                                                Query Match
Best Local (
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                                                                                                                                                                                                 Matches
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                                                                              178 SDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFF-PPEY 234
                                                                                                                                                             118 RVIFITEYVSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLT 177
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                                                               63 CDSIFIQHNGLVKIGSV--
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                 11:23:01
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/USO7_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/USO1_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/USO1_NEW_COMB.pep:*
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US-60-752-355-5150
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US-60-752-355-4268
US-60-752-355-4268
US-60-752-355-35913
US-60-752-355-10912
US-60-752-355-1629
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Sequence 1714, Ap
Sequence 38255, A
Sequence 5150, Ap
Sequence 13134, Ap
Sequence 11780, A
Sequence 11780, A
Sequence 1875, Ap
Sequence 24004, A
Sequence 24004, A
Sequence 30838, A
Sequence 3790, Ap
Sequence 4183, A
Sequence 46137, A
Sequence 40098, A
Sequence 40098, A
Sequence 5142, Ap
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Sequence 5514, A
Sequence 5514, A
Sequence 19114, A
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| AIAR | | DLRS | | RWCT | APL- | -VTQ | SPCG | 3 | 2*; | INE : US -08- US/1 10/0 -18 JP 2 -18 | us/1 | a | œ | œ œ | 7 8 | | 000 | 00 00 | 7 8 | ω ω | œ œ ~ | 1 00 |
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| PNMR | EVINV | ELRN | SHTA: | FLHA | | VKILH | NAC. | matc | 882. No. | .РНАТ ,063 98 789 | A NMER | 2 - 2 | 52-3 | 52-3 | 11-9 | 52-3 | 52-3 | 52-3 | 52-3 11-9 | 52-3 | 11-5 52-3 52-3 | 52-3 |
| BFII | V | LHFF | ĕ- | -8 | | KYWI | RNV. | hes | 1.3e | -B | TS | | ij | អ៊ី អ៊ី | Öÿ | ijij | ijij | ĢĢ | 5 % | 5. 9. | 5 5 6 | ŞΫ́ |
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| H 31 | - 20 | A 25 | - 18 | Н 19 | - 15 | K 13 | н. | 7 1 | | EPTORS | | , Ab | 2 | 4. | , 9 A | 7,4 | 900 | 900 | . `⊍ ≱ . | 96 | App | |
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Sequence 38255, Application US/60752355
(GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with enl
FILE REFERENCE: 38-21(53720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
SOFTWARE: Patentin version 3.3
SEQ ID NO 38255
LENGTH: 554
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; ORGANISM: Oryza sativa
US-60-752-355-38255
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Local Similarity 22.8%;
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VPDPWLEISQLKAP--
                                 LAPPPEEVQKAKTPTPEPFDSETR 426
                                                                                                         RPRRP---PL-QWRYSEVSFMELDKF------LEDVRNGIYPLMNFAATRPLGLPRV
                                                                                                                                                                                                                                         PEVIMNTNGY-----VAAIFKIG 361
                                                                                                                                                                                                                                                                                                                                                                                      LHACSPPIIHGNLTSDTIFIQHNGLIKI---GSVWHRIFSNALRPPTALPDDLRSPIRAE
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                                                                       LPVSPCSSPLRQYRQSNRSCMPSPPHPAYSAGAANYSPINNALYP-----KRP---SNH
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Pred. No. 1.1e-10;
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US-60-752-355-5150
; Sequence 5150, Application US/60752355
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al.
; TITLE OF INVENTION: Transgenic plants with end; FILE REFERENCE: 38-21 (53720);
; CURRENT APPLICATION NUMBER: US/60/752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
                                                                                  US-60-752-355-13134
US-60-752-355-13134
US-60-752-355-13134
Sequence 13134, Application US/60752355
GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with enl
FILE REFERENCE: 38-21(53720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
SOFTWARE: Patentin version 3.3
SEQ ID NO 13134
LENGTH: 894
TYPE: PRT
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; NAME/KEY: misc feature
; LOCATION: (726)..(726)
; OTHER INFORMATION: Xaa
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                                                    ; ORGANISM: Oryza
US-60-752-355-13134
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SEQ ID NO 5150
LENGTH: 833
TYPB: PRT
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                     sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.3%;
                                                                                                                                                                                                                                                                                                                                                                                  -QHPFVQKAVSLEKSVLSE 678
7.3%;
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Score 196;
Pred. No.
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Pred. No. 4e-10;
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 196; DB 8;
No. 4.5e-10;
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                Length 894;
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Sequence 31780, Application US/60752355
(GENERAL INFORMATION:
APPLICAUT: Abad, Mark et al.
ITITLE OF INVENTION: Transgenic plants with enly
FILE REFERENCE: 38-21(53720)B
(CURRENT APPLICATION NUMBER: US/60/752,355
(CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
(SOFTWARE: Patentin version 3.3
(SOFTWARE: Patentin version 3.3
(SEQ ID NO 31780
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US-60-752-355-31780
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature LOCATION: (289)...(289) OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 7.3%;
Local Similarity 25.3%;
    313
                                        607
                                                                                                                    561
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                                                                                                                                                                                                                                                                                                                                                                                         32 SPCGRWQKRREQVNQGNMPGLQSTF----LAMDTEEGVEVVWNE--LHFGDRKAFAAHEE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
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                                                                                                                                                                                                                                HKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSN 201
                                                                                                                                                                                                                                                                          SAKQLGQEISLLSRLQHPNIVQYY-----GSETVDDKLYIYLEYVSGGSIHKLLQE----
                                                                                                                                                                                                                                                                                                            KIQTVFEQLVL---VDHPNIVKLHKYWLDTSEACARVIFI-TEYVSSGSLKQFLKKTKKN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGQLGEQAIRSYTQQILSGLAYLHAKN--TVHRDIKGANILVDPSGRVKLADFGMAKHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSN
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    FEVHSLKLLAAHCFIQHQYLMPENVVEE 340
                                        PPWSQYEGIAAMFKIGNSKELPPIPDHLSEPG-KDFIRKCLQRDPSQRPTAMELL-----
                                                                                                                    GOOCPESPKG---
                                                                                                                                                      ALRPPTALPODLRSPIRAEREELRNLHFFPPEYGEVADG--TAVDIFSFGMCALEMAVLE 259
                                                                                                                                                                                                YGQLGEQAIRSYTQQILSGLAYLHAKN--TVHRDIKGANILVDPSGRVKLADFGMAKHIN
                                                                                                                                                                                                                                                                                                                                                     SPGSRWKK-----GKLIG-RGTFGHVYVGFNSDSGEMCAMKEVTLFLDDPKS----KE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADG--TAVDIFSFGMCALEMAVLE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAKQLGQEISLLSRLQHPNIVQYY-----GSETVDDKLYIYLEYVSGGSIHKLLQE----
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                                                                              ---IQTNGDTRV----TEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFHRVL 312
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                                                                                                                    -ŚP-----YWMAPEVIKNSNGCNLAVDIWŚLGCTVLEMATSK
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 196; DB 8; I
Pred. No. 4.5e-10;
51; Mismatches 112;
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; GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with en
FILE REFERENCE: 38-21(53720)B
; CURRENT PILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11788
; LENGTH: 600
TYPE: PRT
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US-60-752-355-1875
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US-60-752-355-11788
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                    NUMBER OF SEQ ID NOS: 52803
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1875
LENGTH: 611
TYPE: PRT
                                                                                                                                                                                                              Sequence 1875, Application US/60752355 GENERAL INFORMATION:
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Best Local
                                                                                                              APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with
FILE REFERENCE: 38-21(53720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
ORGANISM: Nicotiana benthamiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 7.3%;
Local Similarity 23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 SPCGRWQKRREQVNQGNMPGLQSTF----LAMDTEEG-----VEVVWNELHFGDRKAF 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELP----RPRRPP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMAVLEIQTNGDTRVTEEAIARARHSLSDPNMRE-----FILCCLARDPARRPSAHS 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAHEEKIQTVFEQLVLVD---HPNIVKLHKYWLDTSEACARVIFI-TEYVSSGSLKQFLK 136
                                                                                                                                                                                                                                                                                                                                 SSSPLRR 533
                                                                                                                                                                                                                                                                                                                                                                                                                                               -LOWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMATSKPPWNQYEGVA--AIFKIGNSKDMPEIPEHLSNDAKNFIKLCLQRDPLARPTAHK 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKH-----INSSASMLSFKGSPYWMAPEVVMVTNGY------SLPVDIWSLGCTII 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKI---GS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNVSKWRK-----GKLLG-RGTFGHVYLGFNSENGQMCAIKEVKVVSDD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LL-----SATKAANVSITRDAFPCMFDGSRTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----QHPFVQKAVSLEKSVLSE 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 195.5; DB 8; Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                             -DFASKPALAAPRALRSPRDNTRMITSLPVSP
                                                                                                                                                                            enhanced
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                                                                                                                                                                          agronomic traits
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US-60-752-355-42688
; Sequence 42688, Application US/60752355
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al.
; TITLE OF INVENTION: Transgenic plants with enl
; FILE REFERENCE: 38-21[53720]B
; CURRENT APPLICATION NUMBER: US/60/752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42688
; LENGTH: 567
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                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Oryza sativa
US-60-752-355-42688
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Best Local S
Matches 86
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Best Local Similarity
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                                290
                                                              104 KLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSF 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 ECLKQLNQEIILLSNLSHPNIVRYYGSELDDETLSVYL----EYVSGGSIHKLLQE----
164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 LPVSPTSSPLRQ 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 KWKK-----GKLLG-RGTFGHVYLGFNRENGQMCAIKEVRVVSDD------QTSK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 RWQKRREQVNQGNMPGLQSTF----LAMDTEEG-----VEVVWNELHFGDRKAFAAHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108;
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                                                                                                                                                                                                  2 AAPEPAPRRAREREREEEESEDESDILEESPC-----GRWQKRR-----EQVNQG
                                                                                                                                                                                                                                                    Similarity
LHACSPPIIHGNLTSDTIFIQHNGLIKI----GSVWHRIFSNALRPPTALPDDLRSPIRAE
                                                                                                 FNSEGGQ-----MCAIKEVKVISDD-----SNSKECLRQLHQEIVLLSQLSHPNIV
                                                                                                                              - NMPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVL---VDHPNIV
                                                                                                                                                                   SSPHPLPRP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------VLEIQTNGDTRVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSSSL-----VLSFKGSPYWMAPEVVMNTSGY------GLPVDIWSLGCAILEMASS
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                             QY--YGSDLSSETLSVYL--EYVSGGSIHKLLQE----YGAFGEAVLRNYTAQILSGLAY
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                                                                                                                                                                                                                                 Score 193.5; DB 8;
Pred. No. 3.9e-10;
2; Mismatches 107;
                                                                                                                                                                   -----PGSPCSSSRVVSSQWKKGKLLGSGTFGQVYQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enhanced agronomic traits
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          Sequence 24004, Application US/60752355
(GREERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with en
FILE REFERENCE: 38-21(53720)B
(CURRENT APPLICATION NUMBER: US/60/752,355
(CURRENT FILLING DATE: 2005-12-21
) NUMBER OF SEQ ID NOS: 52803
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24004
LENGTH: 786
TYPE: PRT
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US-60-752-355-24004
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ORGANISM: Zea mays
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APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with en
FILE REFERENCE: 38-21(53720) B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEQ ID NOS: 52803
SOFTMARE: PatentIn version 3.3
SEQ ID NO 35913
LENGTH: 1484
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Sequence 35913, Application US/60752355
GENERAL INFORMATION:
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Best Local Similarity 22.v
Conservative
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1415 GHKPQLPSPEQLSEPGRTFLARCLEHDPTKRPSAVELLADPWMVEIRHM 1463
                                                                                                                                                                                                                                            1298 --VVHRDIKPENVLLDHNGVIKYVDFGAA-KVIASNGRTIGGMTNSSLRKSVKRDGHNNL 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1135 KIEERRRNLQEEFQSIGRVLDVSDSEYQFLTLLASSFSSVSIRWQK-GACIGRGT---FG 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                         109 WLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 STFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDHPNI-----VKLHKY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 RAREREREDESEDESDILEESPCG-----RWOKRREQVNQGNMPGLQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPIIHGNLTSDTIFIQHNGLIK---IGSVWHRIFSNALRPPTALPDDLRSPIRAEREELR
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                                                                                                                                                          NLHFFPPEY--GEVADGTA-----VDIFSFGMCALEMAVLE---IQTNGDTRVTEEAIA
                                                                                                                                                                                                                                                                                                                                                             -----DKVYIFMEFCEGGSLAGLL----THGRIEDEMVIQVYALQMLEGLAYLHQSG 1297
                                                        RARHSLSDPNM-----REFILCCLARDPARRPSAHSLLFHRVLFEVHSL 318
                                                                                                                       NSMTGTPMYMSPEAITGTSTDRSGVVDIWSLGCCVLEMATGRRPWANLDNEWAIMYHIAA
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enhanced agronomic traits

471 306 416 256

421 507

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Sequence 10912, Application US/60752355
(GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with enhanced agriculture of Invention and Invention of Invention Number: US/60/752,355
(CURRENT APPLICATION NUMBER: US/60/752,355
(CURRENT FILING DATE: 2005-12-21
(NUMBER OF SEQ ID NOS: 52803)
(SOFTWARE: Patentin version 3.3)
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US-60-752-355-10912
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US-60-752-355-10912
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 106; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 FLHACSPPIIHGNLTSDTIFIQHNGLIKI---GSVWHRIFSNALRPPTALPDDLRSPIRA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 KLHKYWLDTSEAÇARVIFI-TEYYSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109;
138 TKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 QVYMGFNSEGGOMCAIKEVKVISDD------SNSKESLRQLNQEIVLLSQLSHPNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 SSPQPLP-----GKLLGSGTFG 389
                                                                                                       81
                                                                                                                                                                                                   28 ILEESPC--GRWQKRREQVNQGNMPGLQSTF---LAMDTEEGVEVVWNELH-FGDRKAF
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                                                                                                    AAHEEKIQTVFEQLVLVD---HPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKK
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                                                -TSKECLKQLNQEINLLNQFSHPNIVQY--YGSELGEESLSVYL--EYVSGGSIHKLLQE
                                                                                                                                                     VLENNTCNLSKWKK-----GKLLG-RGTFGHVYLGFNSENGOMCAIKEVKVFSDDK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SSGLTDPWLEISQVKTQT---FDSPRR 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMSLPVSPCSSPLRQYRQSNRSCLRSPPHPAYSAGAANYNPINNALYP-----TRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AELPRPRRP---PL-QWRYSEVSFMELDKF-----LEDVRNGIYPLMNFAATRPLG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHSLSDPN-----MREFILCCLARDPARRPSAHSLLFH----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APEVIMNSNGY-----SLSVDIWSLGCTILEMATAKPPWSQYEGVAAIFK--IGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLE---IQTNGDTRVTEEAIARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPRVLAPPPEEVQKAKTPTPEPFDSETR 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSTDGKNSRVKIETSSYRSLSP---LRDPDILGRNLPGPTSPIPSTSSRRIAALNTSNVR
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                                                                                                                                                                                                                                                            7.1%;
ilarity 24.9%;
Conservative 5:
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                                                                                                                                                                                                                                                       ; Score 190.5; DB 8; 
; Pred. No. 8.8e-10; 
57; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
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GENERAL INFORMATION:
APPLICANT. Abad, Mark et al.
ITILE OF INVENTION: Transgenic plants with enhanced agronomic trailer.
FILE REFERENCE: 38-21(53720)B
CURRENT ETLING DATE: 2005-12-21
INTERNI FILING DATE: 2005-12-21
INTERNI FILING DATE: 2005-13-3
SOFTWARE: Patentin version 3.3
SEQ ID NO 30838
LENGTH: 555
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-60-752-355-30838
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US-60-752-355-30838
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                                                                                                                                                                                                                              211 LITKIHKLIMDPIPAMYSGSFRGLIKSMLRKNPELRPSANELL--
                                                                                                                                                                                                                                                                             272 AIARARHSLSDP------NMREFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAH 324
                                                                                                                                                                                                                                                                                                                                165 GTPS----YMCPELLADIPYGSKSDIWSLGCCMYEMAAHKPPFKASDVQT------
                                                                                                                                                                                                                                                                                                                                                                                 219 AEREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMA-----VLEIQTNGDTRVTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 SALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIR 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508 LEPHSN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 IFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGMCALEMA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 NPFVVEYKDSWVE--KGC-YVCIVIGYCQGGDMTDTIKRACGVH--FPEEKLCQWLVQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 HPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97;
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                                                                      NGIYPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSETRKVIQMQCNLERSE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                       MALDYLH--SNHILHRDVKCSNIFLTKEQDIRLGD----FGLA---KILTSDDLTSSVV
                        RS---
                                                                                                                                                                        CFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRP--PLQWRYSEVSFMELDKFLEDVR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQIGKGS----FGSALLVRHKQBRKKYVLKKIRLARQSDRARRSAHQB-----MELISTVR 59
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                     --SFSNDRRLN-PSVSDTEAGSVSSSGKASPTPM-FNGRKVSEVTVGVVREE 342
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23.3%; Pred. No. 1.8e-09;
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                                                                                                                       -----ISMVYMKLESPRRSTFPLQ
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RESULT 13
US-60-751-420-3790
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US-60-752-355-51629
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US-60-751-420-3790
                                                                           Sequence 51629, Application US/60752355
GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with
FILE REFERENCE: 38-21(3720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3790, Appli
GENERAL INFORMATION
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Matches
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 3790
LENGTH: 544
TYPE: PRT
          NUMBER OF SEQ ID NOS: 52803
SOFTWARE: PatentIn version 3.3
SEQ ID NO 51629
LENGTH: 884
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APPLICANT:
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APPLICANT: Van Eerdewegh, Paul
APPLICANT: Little, Randall David
APPLICANT: Keith, Tim
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Genemap of the human genes associated with Crohn's
FILE REFERENCE: GENI-O11/00US
CURRENT APPLICATION NUMBER: US/60/751,420
CURRENT FILING DATE: 2005-12-19
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 RNTDRORKKSKMTDEETLEKLRSIVSVGDPKKKY-TRFEKIGOG---ASGTVYTALDIAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 7.0%; Score 186; DB 8; Similarity 24.3%; Pred. No. 1.9e-09; 81; Conservative 57; Mismatches 115
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Croteau, Pascal
Allard, Rene
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Paquin, Bruno
Fournier, Helene
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Sequence 18183, Application US/60752355
(GENERAL INFORMATION:
APPLICANT: Abad, Mark et al.
TITLE OF INVENTION: Transgenic plants with en
FILE REFERENCE: 38-21(53720)B
CURRENT APPLICATION NUMBER: US/60/752,355
CURRENT FILING DATE: 2005-12-21
NUMBER OF SEO ID NOS: 52803
SOFTWARE: Patentin version 3.3
SEQ ID NO 18183
LENGTH: 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Arabidopsis thaliana US-60-752-355-18183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-60-752-355-18183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                   Match 6.9%; Score 185.5; DB 8; Local Similarity 24.8%; Pred. No. 4.4e-09;
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                                                                                                                                                                                444 AQQLGQEISVLSRLRHQNIVQYY-----GSETVDDKLYIYLEYVSGGSIYKLLQE----Y
                                                                                                                                                                                                                                                                         395 SPGSRWKK-----GRLLGMGSFGHVYLGFNSESGEMCAMKEVTLCSDDPKS----RES
                                          203 LRPPTALPDDLRSPIRAEREELRNLHFFPPEYGEVADGT--AVDIFSFGMCALEMAVLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 SPCGRWQKRREQVNQGNMPGLQS---TFLAMDTEEGVEVVWNE--LHFGDRKAFAAHEEK 86
                                                                                                                                                                                                                          87 IQTVFEQLVLVD---HPNIVKLHKYWLDTSEACARVIFI-TEYVSSGSLKQFLKKTKKNH 142
                                                                                                                                                                                                                                                                                                                    32 SPCGRWQKRREQVNQGNMPGLQS---TFLAMDTEEGVEVVWNE--LHFGDRKAFAAHEEK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 IQTVFEQLVLVD---HPNIVKLHKYWLDTSEACARVIFI-TEYVSSGSLKQFLKKTKKNH 142
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  QSGPLSFKG---
                                                                                                                                 KAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNA
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                                                                                       GQFGENAIRNYTQQILSGLAYLHAKN--TVHRDIKGANILVDPHGRVKVADFGMAKHITA
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Pred. No. 4e-09;
0; Mismatches 116;
any naturally occurring
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Minimum
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| C;Date: 04- C;Accession R;Koehrer, submitted t. submitted t. A;Reference A;Reference A;Status: p A;Molecule A;Residues: A;Cross refi A;Experimen. C;Genetics: | RESULT T46491 hypoth | 4 2. UJ | 44 | 43 | 42 | 41 | 40 | . w | 37 | 36 | ω S | ω | 33 | 32 | 31 | 30 | |
|--|---|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--|
| C; Date: 04 Feb-2000 #sequence rev: C; Accession: T46491 R; KCehrer, K.; Beyer, A.; Mewes, I submitted to the Protein Sequence A; Reference number: Z23037 A; Accession: T46491 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-258 < AAA> A; Cross-references: UNIPROT:09NSY: A; Experimental source: adult test: A; Experimental source: adult test: C; Genetics: | RESULT 1 146491 hypothetical protein DKFZp434P086.1 | 160.5 | | | 161 | 162 | 162.5 | 16 | | 16 | | 166 | | | 170 | 170 | |
| -Feb-2000 **sequence_re n: T46491 K.; Beyer, A.; Mewes, to the Protein Sequenc e number: Z23037 n: T46491 preliminary type: mRNA : 1-258 <aaa> : 1-258 <aaa> ferences: UNIPROT: QSNS ferences: UNIPROT: QSNS ferences: dull tes</aaa></aaa> | naniens | | | | 6.0 | | 6.1 | | 6.2 | | | | 6.3 | | 6.4 | 6.4 | |
| #sequence_revision , A.; Mewes, H.W.; tein Sequence Datak Z23037 y A AA> UNIPROT:Q9NSY0; UNI | FZp434F | 677 | 722 | 706 | 406 | л : л : | 1895 | 487 | 338 | 746 | 560 | 348 | 348 | 528 | 391 | 372 | |
| rev est | 980 | N | N | N | N | 91 | o N | N | Ŋ | N | N | N | N | N | N | 2 | |
| ision 04-Feb-2000 i i.W.; Gassenhuber, Database, January Database, January Database, January Database, January | | T27127 ALIGNMENTS | T37970 | A48084 | T52626 | T51736 | T15881 | A71407 | JC7838 | 862365 | D85084 | T52635 | T51340 | D86456 | T48115 | T52621 | |
| #text_change 09-Jul-2004 , J.; Wiemann, S. y 2000 9 2000 1006E116; EMBL:AL137662 | - | hypothetical prote | probable G2-specif | STE11 protein kina | probable mitogen-a | mitogen-activated | nrotein kinase 6 (| probable Ste20-lik | Nek6 protein kinas | SNF1-related prote | probable mitogen-a | mitogen-activated | mitogen-activated | probable protein k | protein kinase ATM | mitogen-activated | |

8 밁 δ 밁 S 밁 S 밁 8 Query Match Best Local (Matches 490 181 430 121 370 310 250 MCALEMAVLEIQTNGDTRVTEEAIARARHSLSDPNWREFILCCLARDPARRPSAHSLLFH 241 61 258; _ Similarity KLAAFLESTFLKYRGTQA 507 QMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHEDDRM SFMELDKFLEDVRNGI YPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSETRKVI RVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRPPLQWRYSEV RVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAELPRPRRPPLQMRYSEV KLAAFLESTFLKYRGTQA QMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPTDSAQDLASELVHYGFLHEDDRM SFMELDKFLEDVRNGI YPLMNFAATRPLGLPRVLAPPPEEVQKAKTPTPEPFDSETRKVI MCALEMAVLEIQTNGDTRVTEEAIARARHSLSDPNMREFILCCLARDPARRPSAHSLLFH 50.4%; So larity 100.0%; I Conservative 0; 258 Score 1346; DB 2; ; Pred. No. 2.6e-81; 0; Mismatches 0; Length 258; Indels 0 Gaps 489 429 369 180 120 60 309 0

hypothetical protein H37N21.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T23136; T23575 R; MCMurray, A. submitted to the EMBL Data Library, November 1997 A; Reference number: Z19694

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A;Accession: T23136
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-231 <WIL>
A;Residues: 1-231 <WIL>
A;Residues: 1-231 <WIL>
A;Residues: 1-231 <WIL>
A;Cross-references: UNIPROT:045668; UNIPARC:UPI000076BE3; EMBL:AL008986; PIDN:CAA15621.
A;Cross-references: UNIPROT: D45668; UNIPARC:UPI000076BE3; EMBL:AL008986; PIDN:CAA15621.
A;Cross-references: Z19762
A;Accession: T23575
A;Accession: T23575
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A;Experimental source: clone K10D3
C;Genetics:
A;Gene: CESP:H37N21.1
A;Map position: 1
A;Introns: 31/3; 68/1; 122/3; 152/3; 171/3
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A;Molecule type: DNA
A;Residues: 1-461 <WIL>
A;Cross-references: UNIPROT:Q21419; UNIPARC:UPI000007CFE6; EMBL:
A;Experimental source: clone K10D3
C;Geneeics:
A;Geneeics:
A;Genee: CESP:K10D3.5
A;Map position: 1
A;Introns: 12/1; 40/1; 124/3; 157/3; 212/3; 345/2; 386/3; 421/2
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R;McMurray, A.
Submitted to the EMBL Data Library, June 1996
A;Accession: T23574
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                                                                              PDDLRSPIRAEREELRNLHFFPPEYGEVADGT-AVDIFSFGMCALEMAV---LEIQTNGD
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HAIVDSKKY--EDVSESAFRIKD-NETIAATSKLR----EMAYCQVAAFQVDLEKFLDDV
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; Pred. No. 1.1e-28;
31; Mismatches 45,
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A;Molecule type: DNA
A;Residues: 1-516 <QUE>
A;Cross-references: UNIPROT:Q9STK6; UNIPARC:UPI00000A845D;
A;Experimental source: cultivar Columbia; BAC clone T29H11
C;Genetics:
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A; Introns: 23/3; 36/2; 112/2; 187/1; 239/3; 295/1; 338/1
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A; Accession: T06716
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                                         TRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLPT----
                                                                                      --SEVGLLTVEGQRKDL-NTIFLKLRITDSK-------GQIRNIHFPFNIETDTS
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25.3%; Pred. No. 5.4e-17;
ative 88; Mismatches 176;
                                                                                                                                                                              ----KCYKEN----TENVSSHKENGYNGNGIVDKLSD
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C;Accession: T02951
R;Kim, C.Y.; Cheon, S.Y.; Cho, M.J.
submitted to the EMBL Data Library, July 1998
A;Description: Identification and characterization
A;Reference number: Z14788
A;Accession: T02951
                                                                                    probable mitogen activated protein kinase C,Species: Oryza sativa (rice) C,Date: 24-Mar-1999 #sequence_revision 24-C,Accession: T02951 R;Kim, C,Y.; Cheon, S,Y.; Cho, M.J.
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A;Status: preliminary; translated
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A; Residues: 1-1851 <WIL>
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;Introns: 15/3; 42/1;
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;Experimental source: clone C46C2
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Best Local Similarity
Matches 128; Conserv
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ilarity 25.0%;
Conservative 8
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Pred. No. 4.7e-16;
B; Mismatches 188;
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R;Delseny, M.; Berger, ...
submitted to the Protein So
macronce number: Z23013
                                                            A; Map position: 3
A; Introns: 24/3;
A; Note: T18N14.10
                                                                                                                                                                                                                                                                         MAP kinase - Arabidopsis thaliana
N;Alternate names: protein T18N14.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000
                                                                                                                                                       A; Molecule type:
A; Residues: 1-547
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A;Residues: 1-677 <KIM>
A;Cross-references: UNIPROT:O81637; UNIPARC:UPI00000A443B; EMBL:AF080436; NID:g3450841;
A;Experimental source: cultivar Millyang 117
C;Genetics:
A;Gene: MEK1
                                                                                                                       A;Cross-references: UNIPROT:Q9SCU5; UNIPARC:UPI000009F4A7; A;Experimental source: cultivar Columbia; BAC clone T18N14
                                                                                                                                                                                  A;Accession: T46059
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNALRPPTAL----PDDLRSPIRAEREELRNLHFFPPEYGEVADGTAVDIFSFGMCALE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -HMRVNIWAVKHWCRQILSGLLYLHSHDPPIIHRDLKCDNIFVNGNQGEVKIGDLG---L 176
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                                                                                                                                                                                                                             Berger, C.; Cooke,
he Protein Sequence
                                                                                                                                                                      DNA
                                                                           113/2;
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                                                                           188/1; 240/3;
            12.3%;
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Pred. No. 2.3e
71; Mismatches
Score 327.5; DB 2;
Pred. No. 4.8e-14;
9; Mismatches 176;
                                                                                                                                                                                                                               R.; Grellet, F.; Laudie,
Database, December 1999
                                                                           350/1
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Conservative

79;

Indels

119;

Gaps

23;

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R;Cooke, R.M.; Laudie, M.; Berger, C.; Delseny, M. submitted to the EMBL Data Library, May 1999 A;Description: Analysis of Arabidopsis thaliana gene A;Reference number: Z25297 A;Accession: T51099 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAP kinase [imported] - Arabidopsis thaliana c,Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 C;Accession: T51099 R;Cooke, R.M.; Laudie, M.; Berger, C.; Delseny, M.
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Best Local Similarity
                     172
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                                                      SVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLH-----
                                                                                                                                                          --VFRS-PEPLQRLYSEVHLLKNLNHESIIRYCTSWIDVNRRTFN--FITELFTSGTLRE
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                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                       VDIRAIKSWARQILNGLAYLHGHDPPVIHRDLKCDNIFVNGHLGQVKIG
                                                                                                                                                                                                                                                                                                                    12.3%; Score 327.5; 25.8%; Pred. No. 4.9
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                   GLAAILRGS----QNAHSVIGTPEFMAPELYEEDYNELVDI
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R;Ruiz-Perez, V.L.; Murillo, F.J.; Torres-Martinez, S.
Curr. Genet. 28, 309-316, 1995
A;Title: PkpA, a novel Phycomyces blakesleeanus serine/threonine prot
A;Reference number: S59578; MUID:96120859; PMID:8590476
A;Accession: S59578
A;Accession: S59578
A;Molecule type: DNA
A;Residues: 1-9;39-346 <RUW>
A;Cross-references: UNIPARC:UPI0000172622; UNIPARC:UPI0000172623; EMB
A;Note: only part of the coding region is given
C;Genetics:
A;Gene: pkpA
A;Introns: 60/1; 248/3; 277/2; 339/3; 534/1
C;Superfamily: Phycomyces blakesleeanus probable serine/threonine-spe
C;Keywords: phosphotransferase; protein kinase
F;34-289/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
849611
grobable serine/threonine-specific protein kinase pkpA (EC c)Species: Phycomyces blakesleeanus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_ch
C;Accession: S49611; S59578
R;Ruiz-Perez, V.; Murillo, F.; Torres-Martinez, S.
submitted to the EMBL Data Library, November 1994
A;Bescription: A novel serine/threonine protein kinase in t
A;Reference number: S49611
A;Accession: S49611
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A; Residues: 1-633 < RUI>
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                  CALEMAVLEIQTNGDT-----
                                                                                                                                                          QFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQ-HNGLIKI
                                                                                                                                                                                                                               HFGDRKAFAAHEEKIQTVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLK
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                                                      GDMGTAEMKNGKKYTV----IGTP-----
                                                                                     GSVWHRIFSNALRPPTALPDDLRSPIRAEREELRNLHFFPPE-YGEVADGTAVDIFSFGM
                                                                                                                       EYIRKLT---PLPNIKIVKRWCRQILKGLAYLHGHEPPIIHRDIKCDNIFINGAHGEIKI
                                                                                                                                                                                            EITNVKVTROEFKDLGHEIDILKSVRHPNIITFHDAWYNETE----FVFITELMTSGTLR
                                                                                                                                                                                                                                                                  DMEFVDQSNMPDYEKVIEASGNGRYSKLNTVLGKG---AYKVVYKAIDREEAI----NDN
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                                                                                                                                                                                                                                                                                                                                     Score 316.5; DB 1;
Pred. No. 3.1e-13;
7; Mismatches 193;
-RVTEEAIARARHSLSDPNMREFILCCLARDPARRPSA
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MAP kinase kinase kinase - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 0 C;Accession: T39225

R;Churcher, C.M.; Gentles, S.; Barrell, B.G.; Rajandream, M.A.; W submitted to the EMBL Data Library, August 1997

A;Reference number: Z21837

A;Accession: T39225

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1401 <CHU>
A;Cross-references: UNIPROT:014299; UNIPARC:UPI0000138F13; EMBL:Z A;Experimental source: strain 972h-; cosmid c9G1

C;Genetics:
A;Gene: SPDB:SPAC9G1.02

A;Map position: 1
RASSULT 11
$40482

$40482

Serine/threonine-specific protein kinase (EC 2.7.1.-)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #tc

C;Accession: $40482
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87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLERLNHPNVVTYYGVEVHR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWOKKREOVNOGNM--PGL-OSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIOTVFE
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                                                                                                                                                                                                                                                                                                                                                                                                                             RAWKRWCTQILSALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNAL--RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLVLVDHPNI-----VKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNA 147
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                                                                                                                                                            THPWITDFRKKTIIT
                                                                                                                                                                                            FHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMDLHAVLAE
                                                                                                                                                                                                                                    MTGSTPWSEMDNEWAIMYHVAAMHTPSIPQNEKISSLARDFIEQCFERDPEQRPRAVDLL
                                                                                                                                                                                                                                                                      LEIQTNGDTRVTEEAI----ARARHSLSDPN-----MREFILCCLARDPARRPSAHSLL
                                                                                                                                                                                                                                                                                                              PTD-PEVRYEDIQPELQHLAG----TPMYMAPEIILGTKKGDFGAMDIWSLGCVILEM--
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Pred. No. 8.1e-05;
i0; Mismatches 135;
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                        05-Oct-2004
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SSGSAPSSGGSASSTNTNSSIEAKNYSDLVRGNRIGSGAGGTVYKVIHRPSSRLYALKVI

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RESULT 12
T51339
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DNA Res. 5, 341-348, 1998
A;Title: Molecular cloning and characterization of three cDNAs
A;Reference number: Z25272; MUID:99156228; PMID:10048483
                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitogen-activated protein kinase kinase (EC 2.7.1 N;Alternate names: MAP kinase kinase 4 C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI000017A3E7
C;Keywords: ATP; phosphotransferase; serine/threonine-specific
F;267-520/Domain: protein kinase homology <KIN>
F;275-283/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Manser, E.; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L. Nature 367, 40-46, 1994
A;Title: A brain serine/threonine protein kinase activated A;Reference number: S40482; MUID:94150588; PMID:8107774
                                                                                                               A;Description: (EC 2.7.1.-); mitogen-activated protein kinase kinase [valid C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: phosphotransferase; protein kinase
                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-366 <ICH>
A; Cross-references: UNII
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A; Residues: 1-544 < MAN>
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S
                                                                                                                                                                            C; Function:
                                                                                                                                                                                           A; Gene: ATMKK4
                                                                                                                                                                                                                                 A; Experimental source:
                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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Matches 81
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Similarity 24.6%;
                                                            Similarity
     NQGNMPGLQSTFLAMDTEEGVE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPAPRRAREREREDESEDESDILEE-----SPCGRWQKRREQVNQGNMPGLQST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRDIKSDNILLGMDGSVKLTDFG---FCAQI-----TPEQSKRSTMVGTPYWMA
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                                                                                                                                                                                                                                 strain
                                                                                                                                                                                                                                  Columbia
                                           54;
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                                         Score 190; DB 2;
Pred. No. 3.1e-05;
4; Mismatches 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 191; DB 2;
Pred. No. 4.4e-05;
                                                                                                                                                                                                                                                UNIPARC: UPI000009FE2F; EMBL: AB015315; PIDN: BAA28830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.7.1.-)
                                             122;
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     ----VVWNELHFGDRKAFAA----
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                                                                                                                                                            MUID: 9
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p21-activated protein kinase - human c;Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision C;Accession: G01773
R;Chernoff, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, April 1995 A;Reference number: G08374 A;Accession: G01773
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Best Local S
Matches 84
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 484
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                                 RHSLSDPN-----MREFILCCLARDPARRPSAHSLIFHRVL 312
                                                                                                                                                                                                                                    SEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLHACSPPII 172
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                                                                                                  PPEYGEVADGTAVDIFSFGMCALEM------AVLEIQTNGDTRVTEEAIARA 276
                                                                                                                                 HRDIKSDNILLGMDGSVKLTDFG---FCAQI-----TPEQSKRSTMVGTPYWMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---HEEKIQ----TVFEQLVLVDHPNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFL
                                                                PEVVTRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNG----TPE-----
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ilarity 24.6%;
Conservative 6
ONPEKLSAIFRDFLNRCLDMDVEKRGSAKELLQHQFL 521
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5.1e-05;
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A;McCession: A57441
A;Molecule type: protein
A;Residues: 197-216;402,'S',404-409 <BEN>
A;Cross-references: UNIPARC:UDI000017A3BF; UNIPARC:UDI000017A3C0
A;Experimental source: placenta
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotran
F;247-501/Domain: protein kinase homology <KIN>
E;255-63/Region: protein kinase ATP-binding motif
F;197,402/Binding site: phosphate (Ser) (covalent) #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI000017A3BE R;Benner, G.B.; Dennis, P.B.; Masaracchia, R.A. J. Biol. Chem. 270, 21121-21128, 1995
A;Title: Activation of an 36/H4 kinase (PAK 65)
A;Reference number: A57441; MUID:95403344; PMID:
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EMBO J. 14, 1970-1978, 1995
A;Title: A novel serine kinase activated by rac1/CDC42Hs-dependent autophosphorylation A;Reference number: S55258; MUID:95262637; PMID:7744004
A;Accession: S55258
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N;Alternate names: protein kinase PAK65; S6/H4 kinase
C;Species: Homo sapiens (man)
C;Date: 22-Aug-1996 #sequence revision 06-Sep-1996 #text_change 05-Oct-2004
C;Accession: S58882; S55258; S55304; S58690; A57441
R;Sells, M.; Knause, U.J.; Bagrodia, S.; Ambrose, D.; Bokoch, G.M.; Chernof: submitted to the EMBL Data Library, April 1995
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R;Martin, G.A.; Bollag, G.; McCormick, F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 'MEETQQKSNLEL',31-89,'T',91-149,'F',151-224,'T',226-328,'R',330-338,340-525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-30 < MAF>
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A;Contents: erratum
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A;Accession: S55304
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A; Residues: 1-525 <SEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: not compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S58690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \hat{A}_iDescription: Human p21-activated protein kinases regulate actin organization \hat{A}_iReference number: S58682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
  406
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GTPYWMAPEVVTRKAYGPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQ 465
                                                                                                                                                                                                                                                                                                                                                                                                                                 PVPAPVGDSHVDGAAKSLDKQKKKPKMTDEEIMEKLRTIVSIGDPKKKY-TRYEKIGQG-
                                                       NLHFF--PPEYGEVADGTAVDIFSFGMCALEM-----
                                                                                                                                                                                                                ---FLDSYLVGDELFVVMEYLAGGSLTDVVTETACMDEAQIAAV---
                                                                                                                                                                                                                                                                                                                          --ASGTVFTATDVALGQEVAIKQINL-----QKQPKKELIINEILVMKELKNPNIVN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPAP-----RRAREREREREDESEDESDILEE-----SPCGRWQKRREQVNQGN 48
                                                                                                         A--NOVIHRDIKSDNVLLGMEGSVKLTDFG---FCAQI--
                                                                                                                                                           ACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRAEREELR
                                                                                                                                                                                                                                                               HKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILSALSFLH 165
                                                                                                                                                                                                                                                                                                                                                                            MPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVL---VDHPNIVKL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.0%; Score 188; DB 2;
23.6%; Pred. No. 6.6e-05;
ive 60; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUID:96016211; PMID:7556080
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PMID:7673144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 525;
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                                               AVLEIQTNGDTRVT
                                                                                                      ----TPEQSKRSTMV 405
                                                                                                                                                                                                                -CRECLQALEFIH
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A;Molecule type: mRNA
A;Residues: 1-544 <MAN>
A;Residues: 1-544 <MAN>
A;Residues: 1-544 <MAN>
A;Cross-references: UNIPROT:Q62829; UNIPARC:UPI0000131225; GB:U33314; NID:g1039424; PIDN
C;Keywords: ATP
F;266-519/Domain: protein kinase homology <KIN>
F;274-282/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Manser, E.; Chong, C.; Zhao, Z.S.; Leung, T.; Michael, G.; Hall, C.; Lim, L. J. Biol. Chem. 270, 25070-25078, 1995
A;Title: Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) A;Reference number: A57597; MUID:96027610; PMID:7559638
A;Accession: A57597
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A57597
beta-p21-activated protein kinase - rat
beta-p21-activated protein kinase - rat
N;Alternate names: beta-PAK
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 31-Dec-2004
C;Accession: A57597
Search completed: January 12, 2006, 11:22:27 Job time : 20 secs
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                                                                                                                                                                                                                 18 KRSTMVGTPYWMAPEVVTRKAYGPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATN
                                                                                                                                                                                                                                                                                                                             374 ALDFLH--SNQVIHRDIKSDNILLGMDGSVKLTDFG---FCAQI-----TPEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                       323 PNIVN----YLDSYLVGDELWVVMEYLAGGSLTDVVTET-----CMDEGQIAAVCRECLQ 373
                                                                                                            478
                                                                                                                                                    264 GDTRVTEBAIARARHSLSDPN-----MREFILCCLARDPARRPSAHSLLFHRVL 312
                                                                                                                                                                                                                                                                 220 EREELRNLHFF--PPEYGEVADGTAYDIFSFGMCALEM------AVLEIQTN 263
                                                                                                                                                                                                                                                                                                                                                                                       160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 KIGÓG---ASGTVYTÁLDIATGOEVAIKOMNL------QQQPKKELIINEILVMRENKN 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AAPNKEATPPSAENANSSTLYRNTDRQRKKSKMTDEEILEKLRSIVSVGDPKKKY-TRFE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 NP-----EKLS-PIFRDFLNRCLEMDVEKRGSAKELLQHPFL 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 QVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLV---DH 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AAP--EPAPRRA-----REREREREDESEDESDILEE-----SPCGRWQKRRE 42
                                                                                                       G----TPE-----LQNPERLSAVERDFLNRCLEMDVDRRGSAKELLQHPFL 519
                                                                                                                                                                                                                                                                                                                                                                                    ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALRPPTALPDDLRSPIRA 219
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